

BLAST Basic Local Alignment Search Tool

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Nucleotide Sequence (11111 letters)

Results for: ▼

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|24839

Description

None

Molecule type

nucleic acid

Query Length

11111

SEQ ID NO: 13

Database Name

nr

Description

All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)

Program

BLASTN 2.2.19+ [Citation](#)

Reference

Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

Other reports: [Search Summary](#) [\[Taxonomy reports\]](#) [\[Distance tree of results\]](#)

Search Parameters

Program	blastn
Query range	397-1772
Word size	28
Expect value	10
Hitlist size	100
Match/Mismatch scores	1,-2
Gapcosts	0,0
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

Database

Posted date	Nov 16, 2008 5:48 PM
Number of letters	259,029,644
Number of sequences	7,734,480
Entrez query	none

Karlin-Altschul statistics

Params	Ungapped	Gapped
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Lambda	1.33271	1.28
K	0.620991	0.46
H	1.12409	0.85

Results Statistics

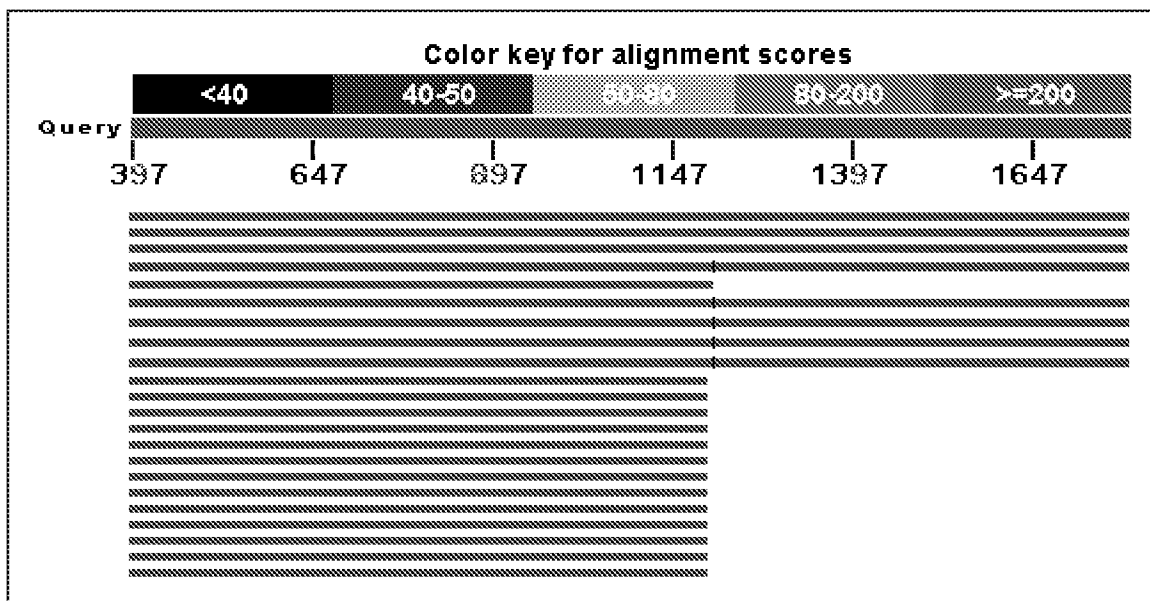
Length adjustment	33
Effective length of query	1343
Effective length of database	25143791804
Effective search space	33768112392772
Effective search space used	33768112392772

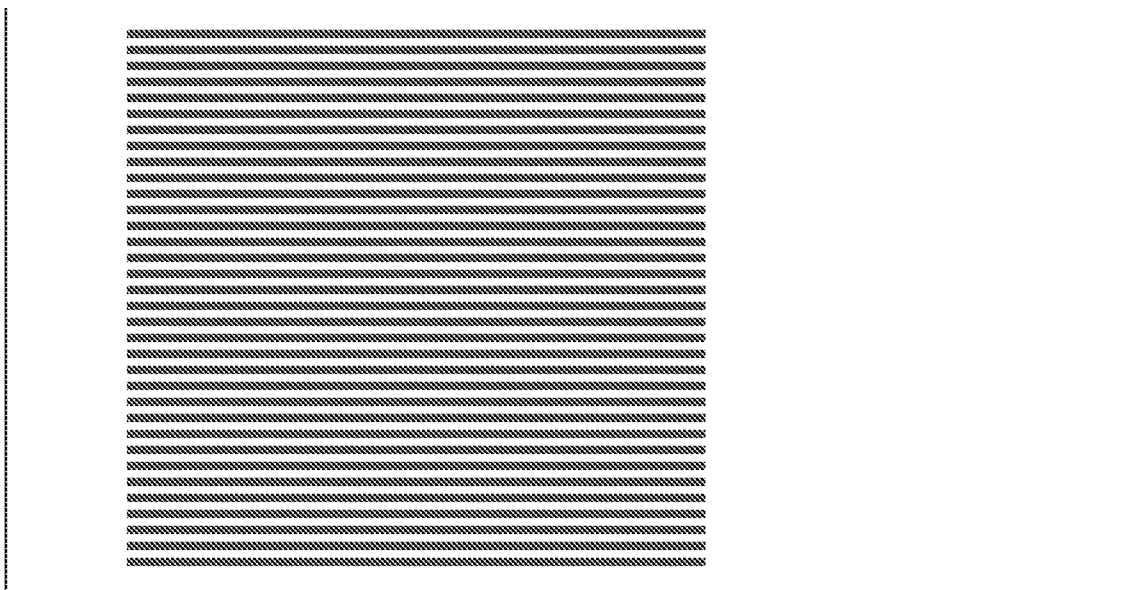
[Graphic Summary](#)

Distribution of 112 Blast Hits on the Query Sequence

?

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





Descriptions

Legend for links to other resources:  UniGene  GEO  Gene  Structure  Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)


AB237837.1	Hepatitis C virus full-length replicon pFGR- JFH1 RNA, complete sequence	2542	2542	100%	0.0	100%
AB114136.1	Hepatitis C virus replicon pSGR-JFH1 gene for neomycin resistance gene product, hepatitis C virus nonstructural protein, complete cds	2542	2542	100%	0.0	100%
AF311318.1	Retroviral vector NIT, complete sequence	2390	2390	99%	0.0	97%
AB119282.1	Hepatitis C virus gene for Fusion protein, Feo, complete cds	1483	2532	100%	0.0	100%
DQ320121.1	Binary vector pBINPLUS/ARS, complete sequence	1483	1483	58%	0.0	100%
AJ242651.1	Hepatitis C virus replicon I377/NS2-3'UTR	1483	2532	100%	0.0	100%
AJ242654.1	Hepatitis C virus replicon I389/NS3-3'UTR	1483	2532	100%	0.0	100%
AJ242653.1	Hepatitis C virus replicon I389/NS2-3'UTR	1483	2532	100%	0.0	100%
AJ242652.1	Hepatitis C virus replicon I377/NS3-3'UTR	1483	2532	100%	0.0	100%
FJ155667.1	Allelic replacement vector pJC84, complete sequence	1471	1471	57%	0.0	100%
AB434475.1	Synthetic construct gfpuv5, aphA genes for green fluorescent protein UV5, kanamycin resistance, complete cds, clone: pT2	1471	1471	57%	0.0	100%
AB434474.1	Synthetic construct gfpuv5, aphA genes for green fluorescent protein UV5, kanamycin resistance, complete cds, clone: pT1	1471	1471	57%	0.0	100%
AB434472.1	Synthetic construct aphA, pyrE, gfpuv5 genes for kanamycin resistance, orotate phosphoribosyltransferase, green fluorescent protein UV5, complete cds, clone: OSU12-pyrE	1471	1471	57%	0.0	100%
AB293446.1	Saccharomyces cerevisiae gene for aquaporin Aqyl, complete cds, clone: COS5	1471	1471	57%	0.0	100%
AB293445.1	Saccharomyces cerevisiae gene for aquaporin Aqyl, complete cds, clone: COS4	1471	1471	57%	0.0	100%
FM162567.1	Trypanosoma brucei Lister 427 surface glycoprotein expression site BES2/TAR129, from bloodstream	1471	1471	57%	0.0	100%
EU491017.1	Suicide vector pEX18Km-pheS, complete sequence	1471	1471	57%	0.0	100%
EU232662.1	Cloning vector pVMGCR85, complete sequence	1471	1471	57%	0.0	100%
EU232661.1	Cloning vector pVMG-TnpR, complete sequence	1471	1471	57%	0.0	100%
AB366441.1	Salmonella enterica subsp. enterica serovar Dublin plasmid pMAK2 DNA, complete genome, strain: L-789	1471	1471	57%	0.0	100%
EU047752.1	Cloning vector pDC8, complete sequence	1471	2177	57%	0.0	100%
EU024548.1	Cloning vector pCPP5250, complete sequence	1471	1471	57%	0.0	100%
EU024546.1	Cloning vector pCPP5702, complete sequence	1471	1471	57%	0.0	100%
EF437956.1	Expression vector pcdNA3-AQP4f, complete sequence	1471	1471	57%	0.0	100%
EF437953.1	Expression vector pcdNA3-AQP4e, complete sequence	1471	1471	57%	0.0	100%
EF437951.1	Expression vector pcdNA3-AQP4d, complete sequence	1471	1471	57%	0.0	100%
EF437950.1		1471	1471	57%	0.0	100%

	Expression vector pcDNA3-K-AQP4d, complete sequence					
CP000744.1	Pseudomonas aeruginosa PA7, complete genome	1471	1471	57%	0.0	100%
AY667410.1	Shuttle cosmid vector pHZ1358, complete sequence	1471	1471	57%	0.0	100%
AM711972.1	Transposon mutagenesis vector pMiET	1471	1471	57%	0.0	100%
EF550208.1	Cloning vector pcDNA3.1+PA, complete sequence	1471	1471	57%	0.0	100%
EF192606.1	Cloning vector pBEO210, complete sequence	1471	1471	57%	0.0	100%
EF028675.1	Cloning vector pDV-NTAP-CYFP, complete sequence	1471	1471	57%	0.0	100%
EF028674.1	Cloning vector pDV-NTAP-CGFP, complete sequence	1471	1471	57%	0.0	100%
EF028673.1	Cloning vector pDV-CYFP-CTAP, complete sequence	1471	1471	57%	0.0	100%
EF028672.1	Cloning vector pDV-CGFP-CTAP, complete sequence	1471	1471	57%	0.0	100%
EF028671.1	Cloning vector pDV-NYFP-CTAP, complete sequence	1471	1471	57%	0.0	100%
EF028670.1	Cloning vector pDV-NTAP-NYFP, complete sequence	1471	1471	57%	0.0	100%
EF028669.1	Cloning vector pDV-CTAP, complete sequence	1471	1471	57%	0.0	100%
EF028668.1	Cloning vector pDV-CYFP, complete sequence	1471	1471	57%	0.0	100%
EF028667.1	Cloning vector pDV-CGFP, complete sequence	1471	1471	57%	0.0	100%
EF028666.1	Cloning vector pDV-NTAP, complete sequence	1471	1471	57%	0.0	100%
EF028665.1	Cloning vector pDV-NYFP, complete sequence	1471	1471	57%	0.0	100%
EF028664.1	Cloning vector EXP5(+), complete sequence	1471	1471	57%	0.0	100%
EF028663.1	Cloning vector EXP4(+), complete sequence	1471	1471	57%	0.0	100%
EF177812.1	Expression vector pUNIV, complete sequence	1471	1471	57%	0.0	100%
EF030522.1	Inducible protein expression vector pReg Neo, complete sequence	1471	1471	57%	0.0	100%
AB255435.1	Escherichia coli plasmid p086A1 DNA, complete sequence	1471	1471	57%	0.0	100%
DQ886588.1	Expression vector pcDNA3-hFIX, complete sequence	1471	1471	57%	0.0	100%
DQ898181.1	Keratinocyte expression vector phPK14H, complete sequence	1471	1471	57%	0.0	100%
DQ823233.1	Expression vector mce4, complete sequence	1471	1471	57%	0.0	100%
DQ823232.1	Expression vector mce3, complete sequence	1471	1471	57%	0.0	100%
DQ823231.1	Expression vector mce2, complete sequence	1471	1471	57%	0.0	100%
DQ487156.1	Flexi vector pF5K CMV-neo, complete sequence	1471	1471	57%	0.0	100%
DQ487155.1	Flexi vector pF5A CMV-neo, complete sequence	1471	1471	57%	0.0	100%
DQ487211.1	Flexi Vector pFN10A (ACT), complete sequence	1471	1471	57%	0.0	100%
DQ515893.1	HIS3/URA3 reporter vector pH3U3, complete sequence	1471	1471	57%	0.0	100%
DQ408591.1	Transposon mutagenesis vector pGI8-STM, complete sequence	1471	1471	57%	0.0	100%
AY817672.1	SIV vector pCLN8, complete sequence	1471	1471	57%	0.0	100%
AY266291.1	Escherichia coli/Mycobacteria shuttle vector pGB9.2, complete sequence	1471	1471	57%	0.0	100%
AY613997.1	Cloning vector pSRalphaneoR, complete sequence	1471	3585	99%	0.0	100%

AY613992.1	Cloning vector pSRalphaneo, complete sequence	1471	1471	57%	0.0	100%
AY286001.1	Cloning vector pHRE1-km, complete sequence	1471	1471	57%	0.0	100%
DQ059989.1	Cloning vector pSCR001, complete sequence	1471	1471	57%	0.0	100%
AY260554.1	Retrotransposon vector MEL/ELM, complete sequence	1471	2495	98%	0.0	100%
AY260553.1	Retrotransposon vector ELM 5, complete sequence	1471	2495	98%	0.0	100%
AY037297.1	Synthetic construct erythromycin resistance protein (erm) gene, partial cds; and streptomycin 3'-phosphotransferase (sph), bleomycin phosphotransferase (ble), neomycin phosphotransferase (nptII), and gentamycin resistance protein (aac) genes, complete cds	1471	1471	57%	0.0	100%
AF264696.2	Cloning vector pFB-ERV, complete sequence	1471	3430	99%	0.0	100%
DQ092437.1	Insertion vector pWSMK-T, complete sequence	1471	1471	57%	0.0	100%
AF504908.1	Cloning vector pBBRT, complete sequence	1471	1471	57%	0.0	100%
AY062236.1	Transformation vector pRLE6, complete sequence	1471	1471	57%	0.0	100%
AF416990.1	Synthetic construct plasmid pcdNA3-Rluc, complete sequence	1471	1471	57%	0.0	100%
AY181092.1	Synthetic construct S1 promoter-nptII gene-S3 terminator cassette	1471	1471	57%	0.0	100%
AY159034.1	Cloning vector pPLEX-4004, complete sequence	1471	1471	57%	0.0	100%
AY159033.1	Cloning vector pPLEX-4003, complete sequence	1471	1471	57%	0.0	100%
AY159032.1	Cloning vector pPLEX-4002, complete sequence	1471	1471	57%	0.0	100%
AY159031.1	Cloning vector pPLEX-4001, complete sequence	1471	1471	57%	0.0	100%
AY159029.1	Cloning vector pPLEX-501, complete sequence	1471	1471	57%	0.0	100%
AY159020.1	Cloning vector pPLEX-505, complete sequence	1471	1471	57%	0.0	100%
AY048743.1	Template plasmid pKD4, complete sequence	1471	1471	57%	0.0	100%
AY237648.1	Cloning vector pHR50, complete sequence	1471	1471	57%	0.0	100%
AY237649.1	Cloning vector pHR3-km, complete sequence	1471	1471	57%	0.0	100%
AY265466.1	Shuttle vector pAM2770, complete sequence	1471	1471	57%	0.0	100%
AF346624.1	RAGE vector pRIG1, complete sequence	1471	1471	57%	0.0	100%
AL671256.1	Trypanosoma brucei VO2 VSG expression site BAC	1471	1471	57%	0.0	100%
AF286462.1	Promoter probe vector pPROBE'-gfp[LVA], complete sequence	1471	1471	57%	0.0	100%
AF286461.1	Promoter probe vector pPROBE-gfp[LVA], complete sequence	1471	1471	57%	0.0	100%
AF286460.1	Promoter probe vector pPROBE'-gfp[ASV], complete sequence	1471	1471	57%	0.0	100%
AF286459.1	Promoter probe vector pPROBE-gfp[ASV], complete sequence	1471	1471	57%	0.0	100%
AF286458.1	Promoter probe vector pPROBE'-gfp[AAV], complete sequence	1471	1471	57%	0.0	100%
AF286457.1	Promoter probe vector pPROBE-gfp[AAV], complete sequence	1471	1471	57%	0.0	100%
AF286456.1	Promoter probe vector pPROBE'-gfp[tagless], complete sequence	1471	1471	57%	0.0	100%
AF286455.1	Promoter probe vector pPROBE-gfp[tagless], complete sequence	1471	1471	57%	0.0	100%
AF286454.1	Promoter probe vector pPROBE-NT', complete	1471	1471	57%	0.0	100%

sequence						
AF286453.1	Promoter probe vector pPROBE-NT, complete sequence	1471	1471	57%	0.0	100%
AY962288.1	Low threshold vector pLTSUB-302, complete sequence	1471	1471	57%	0.0	100%
AY952935.1	Expression vector pFNK-101, complete sequence	1471	1471	57%	0.0	100%
AY952936.1	Expression vector pINV-110, complete sequence	1471	1471	57%	0.0	100%
DQ225747.1	Gene trapping Ds/T-DNA vector pUR224NB, complete sequence	1471	1471	57%	0.0	100%
DQ225746.1	Gene trapping Ds/T-DNA vector pUR224NA, complete sequence	1471	1471	57%	0.0	100%

[Alignments](#) [Select All](#) [Get selected sequences](#) [Distance tree of results](#)

>dbj|AB237837.1|  Hepatitis C virus full-length replicon pFGR-JFH1 RNA, complet
sequence
Length=11111

Score = 2542 bits (1376), Expect = 0.0
Identities = 1376/1376 (100%), Gaps = 0/1376 (0%)
Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
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Sbjct	518	GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
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Sbjct	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	937
Sbjct	878	GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	937
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Sbjct	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT	997
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
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Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1177


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Sbjct  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT  1177
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Query  1298  TTTTGGCAATGTGAGGGCCCGAAACCTGGCCCTGTCTTCTTGACGAGCATTCTAGGGG  1357
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>dbj|AB114136.1| Hepatitis C virus replicon pSGR-JFH1 gene for neomycin resistance
 gene product, hepatitis C virus nonstructural protein,
 complete cds
 Length=8024

Score = 2542 bits (1376), Expect = 0.0
 Identities = 1376/1376 (100%), Gaps = 0/1376 (0%)
 Strand=Plus/Plus

```

Query  398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGCCGCTTGGGTGGAGAGGCTATTTC  457
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Sbjct  398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGCCGCTTGGGTGGAGAGGCTATTTC  457
Query  458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
      |||
Sbjct  458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
Query  518  GCGCAGGGGGCGCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT  577
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Sbjct  518  GCGCAGGGGGCGCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT  577
Query  578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCAGCTGTG  637
      |||
Sbjct  578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCAGCTGTG  637
Query  638  CTCGACGTTGTCACTGAAGCGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
      |||
Sbjct  638  CTCGACGTTGTCACTGAAGCGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
Query  698  GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
      |||
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Query  758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
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Sbjct  758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817

```

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Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAA   877
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Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC   937
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Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
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Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT   1177
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Sbjct   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT   1177

Query   1178  GACGAGTTCTTCTGAGTTTAAACCCTCTCCCTTAACGTTACTGGCCGAAG   1237
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Query   1238  CCGCTTGAATAAGGCCGGTGTGCGTTTGCTATATGTTATTTCCACCATATTGCCGTC   1297
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Query   1418  TCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAGCGACCCTTTCAGGCAGCGGAACCC   1477
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Query   1538  GGCGGCACAACCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCT   1597
        |||
Sbjct   1538  GGCGGCACAACCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCT   1597

Query   1598  CTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCAGAAGGTACCCATTGTATGGG   1657
        |||
Sbjct   1598  CTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCAGAAGGTACCCATTGTATGGG   1657

Query   1658  ATCTGATCTGGGGCCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAACG   1717
        |||
Sbjct   1658  ATCTGATCTGGGGCCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAACG   1717

Query   1718  TCTAGGCCCCCGAACCACGGGGACGTGGTTTTCTTTGAAAAACACGATGATACC   1773
        |||
Sbjct   1718  TCTAGGCCCCCGAACCACGGGGACGTGGTTTTCTTTGAAAAACACGATGATACC   1773

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>gb|AF311318.1|AF311318 Retroviral vector NIT, complete sequence
Length=7607

Score = 2390 bits (1294), Expect = 0.0
Identities = 1370/1401 (97%), Gaps = 28/1401 (1%)
Strand=Plus/Plus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTC   457
        |||
Sbjct   1686  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTC   1745

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
        |||
Sbjct   1746  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   1805

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Query	518	GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	1806	GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	1865
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	637
Sbjct	1866	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	1925
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	1926	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	1985
Query	698	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	1986	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	2045
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	817
Sbjct	2046	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	2105
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	2106	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	2165
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	937
Sbjct	2166	GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	2225
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	997
Sbjct	2226	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	2285
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	2286	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	2345
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	1117
Sbjct	2346	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	2405
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	2406	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	2465
Query	1178	GACGAGTTCTTCTGAG-----T-T----T-----AAAC-----CCTCTCC-CT	1213
Sbjct	2466	GACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGGTTAAACGAATTCGCCCCCTCTCCCTC	2525
Query	1214	-----TAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTA	1270
Sbjct	2526	CCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTA	2585
Query	1271	TATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCC	1330
Sbjct	2586	TATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCC	2645
Query	1331	TGTCCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCT	1390
Sbjct	2646	TGTCCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCT	2705
Query	1391	GTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGT	1450
Sbjct	2706	GTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGT	2765
Query	1451	AGCGACCCCTTTCAGGCAGCGGAACCCCCACCTGGCGACAGGTGCCTCTGCGGCCAAAA	1510
Sbjct	2766	AGCGACCCCTTTCAGGCAGCGGAACCCCCACCTGGCGACAGGTGCCTCTGCGGCCAAAA	2825
Query	1511	GCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTG	1570
Sbjct	2826	GCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTG	2885
Query	1571	GATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGA	1630
Sbjct	2886	GATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGA	2945
Query	1631	TGCCCAGAAGGTACCCCATTTGATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTAC	1690
Sbjct	2946	TGCCCAGAAGGTACCCCATTTGATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTAC	3005

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Query   1691  ATGTGTTTAGTCGAGGTTaaaaaaCGTCTAGGCCCCCGAACCACGGGGACGTGGTTTT 1750
          |||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Sbjct   3006  GTGTGTTTAGTCGAGGTTAAAAAA-CGTCTAGGCCCCCGAACCACGGGGACGTGGTTTT 3064

Query   1751  CCTTTGAAAAACACGATGATA 1771
          |||||||||||||||||||
Sbjct   3065  CCTTTGAAAAACACGATGATA 3085

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>dbj|AB119282.1| Hepatitis C virus gene for Fusion protein, Feo, complete cds
Length=9658

Sort alignments for this
E value Score Percen
Query start position

Score = 1483 bits (803), Expect = 0.0
Identities = 803/803 (100%), Gaps = 0/803 (0%)
Strand=Plus/Plus

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Query   398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGCCGCTTGGGTGGAGAGGCTATTC 457
          |||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Sbjct   2046  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGCCGCTTGGGTGGAGAGGCTATTC 2105

Query   458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          |||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Sbjct   2106  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 2165

Query   518  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAC TG 577
          |||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Sbjct   2166  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAC TG 2225

Query   578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 637
          |||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Sbjct   2226  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 2285

Query   638  CTCGACGTTGTCACTGAAGCGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
          |||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Sbjct   2286  CTCGACGTTGTCACTGAAGCGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 2345

Query   698  GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          |||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Sbjct   2346  GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 2405

Query   758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 817
          |||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Sbjct   2406  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 2465

Query   818  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
          |||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Sbjct   2466  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 2525

Query   878  GAGCATCAGGGGCTCGCGCCAGCCGAAC TGTTGCCAGGCTCAAGGCGCGCATGCCCGAC 937
          |||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Sbjct   2526  GAGCATCAGGGGCTCGCGCCAGCCGAAC TGTTGCCAGGCTCAAGGCGCGCATGCCCGAC 2585

Query   938  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
          |||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Sbjct   2586  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 2645

Query   998  GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          |||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Sbjct   2646  GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 2705

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGGCTGACCGCTTC 1117
          |||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Sbjct   2706  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGGCTGACCGCTTC 2765


Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Sbjct   2766  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 2825

Query   1178  GACGAGTTCTTCTGAGTTTAAAC 1200
          |||||||||||||||||||
Sbjct   2826  GACGAGTTCTTCTGAGTTTAAAC 2848

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Score = 1048 bits (567), Expect = 0.0
Identities = 572/574 (99%), Gaps = 1/574 (0%)
Strand=Plus/Plus

Query	1200	CCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGT	1259
Sbjct	2887	CCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGT	2946
Query	1260	GCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGAATGTGAGGGCCCGG	1319
Sbjct	2947	GCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGAATGTGAGGGCCCGG	3006
Query	1320	AAACCTGGCCCTGTCTTCTTGACGAGCATTCTAGGGGTCTTTCCCCTCTCGCCAAAGGA	1379
Sbjct	3007	AAACCTGGCCCTGTCTTCTTGACGAGCATTCTAGGGGTCTTTCCCCTCTCGCCAAAGGA	3066
Query	1380	ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA	1439
Sbjct	3067	ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA	3126
Query	1440	ACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTC	1499
Sbjct	3127	ACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTC	3186
Query	1500	TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCAGTGCCAC	1559
Sbjct	3187	TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCAGTGCCAC	3246
Query	1560	GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG	1619
Sbjct	3247	GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG	3306
Query	1620	GGGCTGAAGGATGCCCAGAAGGTACCCCATTTGTATGGGATCTGATCTGGGGCCTCGGTGC	1679
Sbjct	3307	GGGCTGAAGGATGCCCAGAAGGTACCCCATTTGTATGGGATCTGATCTGGGGCCTCGGTGC	3366
Query	1680	ACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAGTCTAGGCCCCCGAACCACGGG	1739
Sbjct	3367	ACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAGTCTAGGCCCCCGAACCACGGG	3425
Query	1740	GACGTGGTTTTCTTTGAAAAACACGATGATACC	1773
Sbjct	3426	GACGTGGTTTTCTTTGAAAAACACGATAATACC	3459

>gb|DQ320121.1|  Binary vector pBINPLUS/ARS, complete sequence
Length=12460

Score = 1483 bits (803), Expect = 0.0
Identities = 803/803 (100%), Gaps = 0/803 (0%)
Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	7952	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	8011
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	8012	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	8071
Query	518	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	8072	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	8131
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG	637
Sbjct	8132	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG	8191
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	8192	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	8251
Query	698	GATCTCCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	8252	GATCTCCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	8311
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	817
Sbjct	8312	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	8371
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAA	877

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Sbjct  8372  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 8431
Query  878   GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 937
          |||
Sbjct  8432  GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 8491
Query  938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT 997
          |||
Sbjct  8492  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT 8551
Query  998   GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          |||
Sbjct  8552  GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 8611
Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGGCTGACCGCTTC 1117
          |||
Sbjct  8612  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGGCTGACCGCTTC 8671
Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||
Sbjct  8672  CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT 8731
Query  1178  GACGAGTTCTTCTGAGTTTAAAC 1200
          |||
Sbjct  8732  GACGAGTTCTTCTGAGTTTAAAC 8754
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>emb|AJ242651.1|SSE242651 Hepatitis C virus replicon I377/NS2-3'UTR
Length=8637

Sort alignments for this
E value Score Percen
Query start position

Score = 1483 bits (803), Expect = 0.0
Identities = 803/803 (100%), Gaps = 0/803 (0%)
Strand=Plus/Plus

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Query  398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
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Sbjct  387  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 446
Query  458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          |||
Sbjct  447  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 506
Query  518  GCGCAGGGGGCGCCCGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT 577
          |||
Sbjct  507  GCGCAGGGGGCGCCCGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT 566
Query  578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 637
          |||
Sbjct  567  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 626
Query  638  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
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Sbjct  627  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 686
Query  698  GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          |||
Sbjct  687  GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 746
Query  758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 817
          |||
Sbjct  747  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 806
Query  818  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
          |||
Sbjct  807  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 866
Query  878  GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 937
          |||
Sbjct  867  GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 926
Query  938  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT 997
          |||
Sbjct  927  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT 986
Query  998  GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          |||
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Sbjct	987	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1046
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	1117
Sbjct	1047	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	1106
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	1107	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1166
Query	1178	GACGAGTTCTTCTGAGTTTAAAC	1200
Sbjct	1167	GACGAGTTCTTCTGAGTTTAAAC	1189

Score = 1048 bits (567), Expect = 0.0
 Identities = 572/574 (99%), Gaps = 1/574 (0%)
 Strand=Plus/Plus

Query	1200	CCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGAATAAGGCCGGTGT	1259
Sbjct	1228	CCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGAATAAGGCCGGTGT	1287
Query	1260	GCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGG	1319
Sbjct	1288	GCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGG	1347
Query	1320	AAACCTGGCCCTGTCTTCTTGACGAGCATTCTAGGGGTCTTTCCCTCTCGCCAAAGGA	1379
Sbjct	1348	AAACCTGGCCCTGTCTTCTTGACGAGCATTCTAGGGGTCTTTCCCTCTCGCCAAAGGA	1407
Query	1380	ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA	1439
Sbjct	1408	ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA	1467
Query	1440	ACAACGTCTGTAGCGACCCCTTTCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTC	1499
Sbjct	1468	ACAACGTCTGTAGCGACCCCTTTCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTC	1527
Query	1500	TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCAGTGCCAC	1559
Sbjct	1528	TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCAGTGCCAC	1587
Query	1560	GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG	1619
Sbjct	1588	GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG	1647
Query	1620	GGGCTGAAGGATGCCCAGAAGGTACCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC	1679
Sbjct	1648	GGGCTGAAGGATGCCCAGAAGGTACCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC	1707
Query	1680	ACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAGCGTCTAGGCCCCCGAACCACGGG	1739
Sbjct	1708	ACATGCTTTACATGTGTTTAGTCGAGGTTAAAAA-CGTCTAGGCCCCCGAACCACGGG	1766
Query	1740	GACGTGGTTTTCTTTTGAAAAACACGATGATACC	1773
Sbjct	1767	GACGTGGTTTTCTTTTGAAAAACACGATAATACC	1800

>emb|AJ242654.1|SSE242654 Hepatitis C virus replicon I389/NS3-3'UTR
 Length=8001

Sort alignments for this
 E value Score Percen
 Query start position

Score = 1483 bits (803), Expect = 0.0
 Identities = 803/803 (100%), Gaps = 0/803 (0%)
 Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	399	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	458
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	459	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	518
Query	518	GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577

Sbjct	519	 GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	578
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG	637
Sbjct	579	 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG	638
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	639	 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	698
Query	698	GATCTCCTGTGCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	699	 GATCTCCTGTGCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	758
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	817
Sbjct	759	 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	818
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	819	 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	878
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC	937
Sbjct	879	 GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC	938
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	997
Sbjct	939	 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	998
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	999	 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1058
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	1117
Sbjct	1059	 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	1118
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	1119	 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1178
Query	1178	GACGAGTTCTTCTGAGTTTAAAC 1200	
Sbjct	1179	 GACGAGTTCTTCTGAGTTTAAAC 1201	

Score = 1048 bits (567), Expect = 0.0
 Identities = 572/574 (99%), Gaps = 1/574 (0%)
 Strand=Plus/Plus

Query	1200	CCCTCTCCCTTCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGT	1259
Sbjct	1240	 CCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGT	1299
Query	1260	GCGTTTGTCTATATGTTATTTTCACCATATTGCCGTCTTTTGGAATGTGAGGGCCCGG	1319
Sbjct	1300	 GCGTTTGTCTATATGTTATTTTCACCATATTGCCGTCTTTTGGAATGTGAGGGCCCGG	1359
Query	1320	AAACCTGGCCCTGTCTTCTTGACGAGCATTCTAGGGGTCTTTCCCTCTCGCCAAAGGA	1379
Sbjct	1360	 AAACCTGGCCCTGTCTTCTTGACGAGCATTCTAGGGGTCTTTCCCTCTCGCCAAAGGA	1419
Query	1380	ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA	1439
Sbjct	1420	 ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA	1479
Query	1440	ACAACGTCTGTAGCGACCCTTTGAGGCAGCGGAACCCCCACCTGGCGACAGGTGCCTC	1499
Sbjct	1480	 ACAACGTCTGTAGCGACCCTTTGAGGCAGCGGAACCCCCACCTGGCGACAGGTGCCTC	1539
Query	1500	TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCAGTGCCAC	1559
Sbjct	1540	 TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCAGTGCCAC	1599
Query	1560	GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG	1619
Sbjct	1600	 GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG	1659


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Query 1620 GGGCTGAAGGATGCCCAGAAGGTACCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC 1679
          |||
Sbjct 1660 GGGCTGAAGGATGCCCAGAAGGTACCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC 1719

Query 1680 ACATGCTTTACATGTGTTTAGTCGAGGTT*****CGTCTAGGCCCCCCGAACCACGGG 1739
          |||
Sbjct 1720 ACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAA-CGTCTAGGCCCCCCGAACCACGGG 1778

Query 1740 GACGTGGTTTTTCCTTTGAAAAACACGATGATACC 1773
          |||
Sbjct 1779 GACGTGGTTTTTCCTTTGAAAAACACGATAATACC 1812

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>emb|AJ242653.1|SSE242653 Hepatitis C virus replicon I389/NS2-3'UTR
Length=8649

Sort alignments for this
E value Score Percen
Query start position

Score = 1483 bits (803), Expect = 0.0
Identities = 803/803 (100%), Gaps = 0/803 (0%)
Strand=Plus/Plus

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Query 398 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
          |||
Sbjct 399 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 458

Query 458 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          |||
Sbjct 459 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 518

Query 518 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577
          |||
Sbjct 519 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 578

Query 578 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 637
          |||
Sbjct 579 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 638

Query 638 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
          |||
Sbjct 639 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 698

Query 698 GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          |||
Sbjct 699 GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 758

Query 758 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 817
          |||
Sbjct 759 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 818

Query 818 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
          |||
Sbjct 819 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 878

Query 878 GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC 937
          |||
Sbjct 879 GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC 938

Query 938 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
          |||
Sbjct 939 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 998

Query 998 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          |||
Sbjct 999 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1058

Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 1117
          |||
Sbjct 1059 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 1118

Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||
Sbjct 1119 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1178

Query 1178 GACGAGTTCTTCTGAGTTTAAAC 1200
          |||
Sbjct 1179 GACGAGTTCTTCTGAGTTTAAAC 1201

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Score = 1048 bits (567), Expect = 0.0
 Identities = 572/574 (99%), Gaps = 1/574 (0%)
 Strand=Plus/Plus

Query	1200	CCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGT	1259
Sbjct	1240	CCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGT	1299
Query	1260	GCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGAATGTGAGGGCCCGG	1319
Sbjct	1300	GCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGAATGTGAGGGCCCGG	1359
Query	1320	AAACCTGGCCCTGTCTTCTTGACGAGCATTCTAGGGGTCTTTCCCCTCTCGCCAAAGGA	1379
Sbjct	1360	AAACCTGGCCCTGTCTTCTTGACGAGCATTCTAGGGGTCTTTCCCCTCTCGCCAAAGGA	1419
Query	1380	ATGCAAGGTCTGTTGAATGTCTGTAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA	1439
Sbjct	1420	ATGCAAGGTCTGTTGAATGTCTGTAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA	1479
Query	1440	ACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTC	1499
Sbjct	1480	ACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTC	1539
Query	1500	TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCAGTGCCAC	1559
Sbjct	1540	TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCAGTGCCAC	1599
Query	1560	GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG	1619
Sbjct	1600	GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG	1659
Query	1620	GGGCTGAAGGATGCCCAGAAGGTACCCCATTTGTATGGGATCTGATCTGGGGCCTCGGTGC	1679
Sbjct	1660	GGGCTGAAGGATGCCCAGAAGGTACCCCATTTGTATGGGATCTGATCTGGGGCCTCGGTGC	1719
Query	1680	ACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAGTCTAGGCCCCCGAACCACGGG	1739
Sbjct	1720	ACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAGTCTAGGCCCCCGAACCACGGG	1778
Query	1740	GACGTGGTTTTCTTTGAAAAACACGATGATACC	1773
Sbjct	1779	GACGTGGTTTTCTTTGAAAAACACGATAATACC	1812

>emb|AJ242652.1|SSE242652 Hepatitis C virus replicon I377/NS3-3'UTR
 Length=7989

Sort alignments for this
 E value Score Percen
 Query start position

Score = 1483 bits (803), Expect = 0.0
 Identities = 803/803 (100%), Gaps = 0/803 (0%)
 Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGCCGCTTGGGTGGAGAGGCTATTTC	457
Sbjct	387	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGCCGCTTGGGTGGAGAGGCTATTTC	446
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	447	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	506
Query	518	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	507	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	566
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTTGCGCAGCTGTG	637
Sbjct	567	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTTGCGCAGCTGTG	626
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	627	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	686
Query	698	GATCTCCTGTCTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	687	GATCTCCTGTCTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	746

Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	817
Sbjct	747	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	806
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAA	877
Sbjct	807	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAA	866
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC	937
Sbjct	867	GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC	926
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	997
Sbjct	927	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	986
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	987	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1046
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	1117
Sbjct	1047	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	1106
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	1107	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1166
Query	1178	GACGAGTTCTTCTGAGTTTAAAC	1200
Sbjct	1167	GACGAGTTCTTCTGAGTTTAAAC	1189

Score = 1048 bits (567), Expect = 0.0
Identities = 572/574 (99%), Gaps = 1/574 (0%)
Strand=Plus/Plus

Query	1200	CCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGT	1259
Sbjct	1228	CCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGT	1287
Query	1260	GCGTTTGCTATATGTTATTTCCACCATATTGCCGCTTTTGGCAATGTGAGGGCCCGG	1319
Sbjct	1288	GCGTTTGCTATATGTTATTTCCACCATATTGCCGCTTTTGGCAATGTGAGGGCCCGG	1347
Query	1320	AAACCTGGCCCTGTCTTCTTGACGAGCATTCTAGGGGTCTTTCCCTCTCGCCAAAGGA	1379
Sbjct	1348	AAACCTGGCCCTGTCTTCTTGACGAGCATTCTAGGGGTCTTTCCCTCTCGCCAAAGGA	1407
Query	1380	ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA	1439
Sbjct	1408	ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA	1467
Query	1440	ACAACGTCTGTAGCGACCCTTTGAGGCAGCGGAACCCCCACCTGGCGACAGGTGCCTC	1499
Sbjct	1468	ACAACGTCTGTAGCGACCCTTTGAGGCAGCGGAACCCCCACCTGGCGACAGGTGCCTC	1527
Query	1500	TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCAGTGCCAC	1559
Sbjct	1528	TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCAGTGCCAC	1587
Query	1560	GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG	1619
Sbjct	1588	GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG	1647
Query	1620	GGGCTGAAGGATGCCAGAAGGTACCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC	1679
Sbjct	1648	GGGCTGAAGGATGCCAGAAGGTACCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC	1707
Query	1680	ACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAGCGTCTAGGCCCCCGAACCACGGG	1739
Sbjct	1708	ACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAGCGTCTAGGCCCCCGAACCACGGG	1766
Query	1740	GACGTGGTTTTCTTTGAAAAACACGATGATACC	1773
Sbjct	1767	GACGTGGTTTTCTTTGAAAAACACGATAATACC	1800

>gb|FJ155667.1| Allelic replacement vector pJC84, complete sequence

Length=3775

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	2313	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	2254
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	2253	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	2194
Query	518	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT	577
Sbjct	2193	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT	2134
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	637
Sbjct	2133	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	2074
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	2073	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	2014
Query	698	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	2013	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	1954
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	817
Sbjct	1953	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	1894
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	1893	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	1834
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC	937
Sbjct	1833	GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC	1774
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	997
Sbjct	1773	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	1714
Query	998	GGCCGCTTTTCTGGATTCAATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	1713	GGCCGCTTTTCTGGATTCAATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1654
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	1117
Sbjct	1653	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	1594
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	1593	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	1534
Query	1178	GACGAGTTCTTCTGAG	1193
Sbjct	1533	GACGAGTTCTTCTGAG	1518

>dbj|AB434475.1| Synthetic construct gfpuv5, aphA genes for green fluorescent protein UV5, kanamycin resistance, complete cds, clone: pT2
Length=2773

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	1485	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	1544
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	1545	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	1604
Query	518	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT	577

Sbjct	1605	 GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	1664
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG	637
Sbjct	1665	 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG	1724
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	1725	 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	1784
Query	698	GATCTCCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	1785	 GATCTCCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	1844
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	817
Sbjct	1845	 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	1904
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	1905	 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	1964
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC	937
Sbjct	1965	 GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC	2024
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	997
Sbjct	2025	 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	2084
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	2085	 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	2144
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	1117
Sbjct	2145	 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	2204
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	2205	 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	2264
Query	1178	GACGAGTTCTTCTGAG 1193	
Sbjct	2265	 GACGAGTTCTTCTGAG 2280	

>dbj|AB434474.1| Synthetic construct gfpuv5, aphA genes for green fluorescent protein UV5, kanamycin resistance, complete cds, clone: pT1
Length=3068

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTC	457
Sbjct	1780	 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTC	1839
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	1840	 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	1899
Query	518	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	1900	 GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	1959
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG	637
Sbjct	1960	 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG	2019
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	2020	 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	2079
Query	698	GATCTCCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	2080	 GATCTCCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	2139

Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	817
Sbjct	2140	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	2199
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	2200	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	2259
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	937
Sbjct	2260	GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	2319
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	997
Sbjct	2320	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	2379
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	2380	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	2439
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	1117
Sbjct	2440	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	2499
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	2500	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	2559
Query	1178	GACGAGTTCTTCTGAG	1193
Sbjct	2560	GACGAGTTCTTCTGAG	2575

>dbj|AB434472.1| Synthetic construct aphA, pyrE, gfpuv5 genes for kanamycin resi
 orotate phosphoribosyltransferase, green fluorescent
 protein UV5, complete cds, clone: OSU12-pyrE
 Length=4263


Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTC	457
Sbjct	1289	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTC	1230
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	1229	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	1170
Query	518	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT	577
Sbjct	1169	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT	1110
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	637
Sbjct	1109	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	1050
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	1049	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	990
Query	698	GATCTCCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	989	GATCTCCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	930
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	817
Sbjct	929	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	870
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	869	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	810
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	937
Sbjct	809	GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	750
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	997

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Sbjct  749  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT  690
Query  998  GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
      |||
Sbjct  689  GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  630
Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
      |||
Sbjct  629  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  570
Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT  1177
      |||
Sbjct  569  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT  510
Query  1178  GACGAGTTCTTCTGAG  1193
      |||
Sbjct  509  GACGAGTTCTTCTGAG  494

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>dbj|AB293446.1|  Saccharomyces cerevisiae gene for aquaporin Aqy1, complete cd
clone: COS5
Length=45016


Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query  398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
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Sbjct  42231  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  42290
Query  458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
      |||
Sbjct  42291  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  42350
Query  518  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
      |||
Sbjct  42351  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  42410
Query  578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
      |||
Sbjct  42411  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  42470
Query  638  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
      |||
Sbjct  42471  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  42530
Query  698  GATCTCCTGTCTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
      |||
Sbjct  42531  GATCTCCTGTCTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  42590
Query  758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC  817
      |||
Sbjct  42591  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC  42650
Query  818  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
      |||
Sbjct  42651  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  42710
Query  878  GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC  937
      |||
Sbjct  42711  GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC  42770
Query  938  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT  997
      |||
Sbjct  42771  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT  42830
Query  998  GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
      |||
Sbjct  42831  GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  42890
Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
      |||
Sbjct  42891  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  42950
Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT  1177
      |||
Sbjct  42951  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT  43010

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Query 1178 GACGAGTTCTTCTGAG 1193
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Sbjct 43011 GACGAGTTCTTCTGAG 43026
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>dbj|AB293445.1|  *Saccharomyces cerevisiae* gene for aquaporin Aqyl, complete cd
clone: COS4
Length=43682

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

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Query 398 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
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Sbjct 4394 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 4335

Query 458 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          |||||
Sbjct 4334 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 4275

Query 518 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577
          |||||
Sbjct 4274 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 4215

Query 578 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG 637
          |||||
Sbjct 4214 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG 4155

Query 638 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
          |||||
Sbjct 4154 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 4095

Query 698 GATCTCCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          |||||
Sbjct 4094 GATCTCCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 4035

Query 758 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 817
          |||||
Sbjct 4034 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 3975

Query 818 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
          |||||
Sbjct 3974 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 3915

Query 878 GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC 937
          |||||
Sbjct 3914 GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC 3855


Query 938 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
          |||||
Sbjct 3854 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 3795

Query 998 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          |||||
Sbjct 3794 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 3735

Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 1117
          |||||
Sbjct 3734 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 3675

Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||||
Sbjct 3674 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 3615

Query 1178 GACGAGTTCTTCTGAG 1193
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Sbjct 3614 GACGAGTTCTTCTGAG 3599
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>emb|FM162567.1|  *Trypanosoma brucei* Lister 427 surface glycoprotein expression
site BES2/TAR129, from bloodstream
Length=51758

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus


Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	1005	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	1064
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	1065	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	1124
Query	518	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	1125	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	1184
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	637
Sbjct	1185	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	1244
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	1245	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	1304
Query	698	GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	1305	GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	1364
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	817
Sbjct	1365	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	1424
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	1425	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	1484
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC	937
Sbjct	1485	GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC	1544
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	997
Sbjct	1545	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	1604
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	1605	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1664
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	1117
Sbjct	1665	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	1724
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	1725	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	1784
Query	1178	GACGAGTTCTTCTGAG	1193
Sbjct	1785	GACGAGTTCTTCTGAG	1800

>gb|EU491017.1| Suicide vector pEX18Km-pheS, complete sequence
Length=5161

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	4767	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	4708
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	4707	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	4648
Query	518	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	4647	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	4588
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	637
Sbjct	4587	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	4528

Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	4527	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	4468
Query	698	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	4467	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	4408
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCACCAAGCGAAACATCGC	817
Sbjct	4407	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCACCAAGCGAAACATCGC	4348
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	4347	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	4288
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	937
Sbjct	4287	GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	4228
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	997
Sbjct	4227	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	4168
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	4167	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	4108
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	1117
Sbjct	4107	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	4048
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	4047	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	3988
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Sbjct	3987	GACGAGTTCTTCTGAG	3972

>gb|EU232662.1|  Cloning vector pVMGCR85, complete sequence
Length=11368

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTC	457
Sbjct	3541	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTC	3600
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	3601	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	3660
Query	518	GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	3661	GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	3720
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	637
Sbjct	3721	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	3780
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	3781	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	3840
Query	698	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	3841	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	3900
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCACCAAGCGAAACATCGC	817
Sbjct	3901	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCACCAAGCGAAACATCGC	3960
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	3961	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	4020

Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAAC	TGTTGCGCCAGGCTCAAGGCGCGCATGCCCCGAC	937
Sbjct	4021	GAGCATCAGGGGCTCGCGCCAGCCGAAC	TGTTGCGCCAGGCTCAAGGCGCGCATGCCCCGAC	4080
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	997	
Sbjct	4081	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	4140	
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057	
Sbjct	4141	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	4200	
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	1117	
Sbjct	4201	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	4260	
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1177	
Sbjct	4261	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	4320	
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Sbjct	4321	GACGAGTTCTTCTGAG	4336	


>gb|EU232661.1| Cloning vector pVMG-TnpR, complete sequence
Length=7264

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	3019	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	3078
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	3079	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	3138
Query	518	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	3139	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	3198
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG	637
Sbjct	3199	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG	3258
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	3259	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	3318
Query	698	GATCTCCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	3319	GATCTCCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	3378
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	817
Sbjct	3379	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	3438
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	3439	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	3498
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAAC	937
Sbjct	3499	GAGCATCAGGGGCTCGCGCCAGCCGAAC	3558
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	997
Sbjct	3559	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	3618
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	3619	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	3678
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	1117
Sbjct	3679	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	3738

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Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
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Sbjct 3739 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 3798

Query 1178 GACGAGTTCTTCTGAG 1193
          |||
Sbjct 3799 GACGAGTTCTTCTGAG 3814
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>dbj|AB366441.1|  Salmonella enterica subsp. enterica serovar Dublin plasmid pM DNA, complete genome, strain: L-789
Length=61571

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query 398 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
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Sbjct 10076 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 10135

Query 458 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          |||
Sbjct 10136 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 10195

Query 518 GCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGTGA 577
          |||
Sbjct 10196 GCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGTGA 10255

Query 578 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTG 637
          |||
Sbjct 10256 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTG 10315

Query 638 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
          |||
Sbjct 10316 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 10375

Query 698 GATCTCCTGTCACTACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          |||
Sbjct 10376 GATCTCCTGTCACTACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 10435

Query 758 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 817
          |||
Sbjct 10436 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 10495

Query 818 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
          |||
Sbjct 10496 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 10555

Query 878 GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 937
          |||
Sbjct 10556 GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 10615


Query 938 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT 997
          |||
Sbjct 10616 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT 10675

Query 998 GGCCGCTTTTCTGGATTATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          |||
Sbjct 10676 GGCCGCTTTTCTGGATTATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 10735

Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 1117
          |||
Sbjct 10736 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 10795

Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||
Sbjct 10796 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 10855

Query 1178 GACGAGTTCTTCTGAG 1193
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Sbjct 10856 GACGAGTTCTTCTGAG 10871
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>gb|EU047752.1|  Cloning vector pDC8, complete sequence
Length=11987

Sort alignments for this
E value Score Percen
Query start position

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	7100	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	7159
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	7160	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	7219
Query	518	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	7220	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	7279
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	637
Sbjct	7280	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	7339
Query	638	CTCGACGTTGTCACTGAAGCGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	7340	CTCGACGTTGTCACTGAAGCGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	7399
Query	698	GATCTCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	7400	GATCTCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	7459
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	817
Sbjct	7460	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	7519
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	7520	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	7579
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC	937
Sbjct	7580	GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC	7639
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	997
Sbjct	7640	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	7699
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	7700	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	7759
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	1117
Sbjct	7760	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	7819
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	7820	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	7879
Query	1178	GACGAGTTCTTCTGAG	1193
Sbjct	7880	GACGAGTTCTTCTGAG	7895

Score = 706 bits (382), Expect = 0.0
Identities = 382/382 (100%), Gaps = 0/382 (0%)
Strand=Plus/Minus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	11249	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	11190
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	11189	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	11130
Query	518	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	11129	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	11070

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Query 578 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTG 637
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Sbjct 11069 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTG 11010

Query 638 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
      |||
Sbjct 11009 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 10950

Query 698 GATCTCCTGTCTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
      |||
Sbjct 10949 GATCTCCTGTCTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 10890

Query 758 CGGCGGCTGCATACGCTTGATC 779
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Sbjct 10889 CGGCGGCTGCATACGCTTGATC 10868
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>gb|EU024548.1| Cloning vector pCPP5250, complete sequence
Length=5155

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query 398 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
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Sbjct 2347 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 2406

Query 458 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
      |||
Sbjct 2407 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 2466

Query 518 GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577
      |||
Sbjct 2467 GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 2526

Query 578 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTG 637
      |||
Sbjct 2527 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTG 2586

Query 638 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
      |||
Sbjct 2587 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 2646

Query 698 GATCTCCTGTCTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
      |||
Sbjct 2647 GATCTCCTGTCTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 2706

Query 758 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCACCAAGCGAAACATCGC 817
      |||
Sbjct 2707 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCACCAAGCGAAACATCGC 2766

Query 818 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAA 877
      |||
Sbjct 2767 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAA 2826

Query 878 GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 937
      |||
Sbjct 2827 GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 2886

Query 938 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT 997
      |||
Sbjct 2887 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT 2946

Query 998 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
      |||
Sbjct 2947 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 3006

Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 1117
      |||
Sbjct 3007 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 3066

Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
      |||
Sbjct 3067 CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT 3126

Query 1178 GACGAGTTCTTCTGAG 1193
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Sbjct 3127 GACGAGTTCTTCTGAG 3142
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>gb|EU024546.1| Cloning vector pCPP5702, complete sequence
Length=8791

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	2827	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	2768
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	2767	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	2708
Query	518	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	2707	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	2648
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	637
Sbjct	2647	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	2588
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	2587	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	2528
Query	698	GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	2527	GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	2468
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	817
Sbjct	2467	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	2408
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	2407	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	2348
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC	937
Sbjct	2347	GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC	2288
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	997
Sbjct	2287	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	2228
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	2227	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	2168
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	1117
Sbjct	2167	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	2108
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	2107	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	2048
Query	1178	GACGAGTTCTTCTGAG 1193	
Sbjct	2047	GACGAGTTCTTCTGAG 2032	

>gb|EF437956.1| Expression vector pcDNA3-AQP4f, complete sequence
Length=6510

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	3215	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	3274
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	3275	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	3334

Query	518	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	3335	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	3394
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	637
Sbjct	3395	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	3454
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	3455	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	3514
Query	698	GATCTCCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	3515	GATCTCCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	3574
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCACCAAGCGAAACATCGC	817
Sbjct	3575	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCACCAAGCGAAACATCGC	3634
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	3635	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTGTCGATCAGGATGATCTGGACGAA	3694
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC	937
Sbjct	3695	GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC	3754
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	997
Sbjct	3755	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	3814
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	3815	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	3874
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	1117
Sbjct	3875	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	3934
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	3935	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	3994
Query	1178	GACGAGTTCTTCTGAG 1193	
Sbjct	3995	GACGAGTTCTTCTGAG 4010	

>gb|EF437953.1| Expression vector pcDNA3-AQP4e, complete sequence
Length=6675

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTC	457
Sbjct	3380	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTC	3439
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	3440	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	3499
Query	518	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	3500	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	3559
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	637
Sbjct	3560	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	3619
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	3620	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	3679
Query	698	GATCTCCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	3680	GATCTCCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	3739

Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	817
Sbjct	3740	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	3799
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAA	877
Sbjct	3800	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAA	3859
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC	937
Sbjct	3860	GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC	3919
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	997
Sbjct	3920	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	3979
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	3980	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	4039
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	1117
Sbjct	4040	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	4099
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	4100	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	4159
Query	1178	GACGAGTTCTTCTGAG	1193
Sbjct	4160	GACGAGTTCTTCTGAG	4175

>gb|EF437951.1| Expression vector pcDNA3-AQP4d, complete sequence
Length=6349

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	3054	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	3113
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	3114	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	3173
Query	518	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	3174	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	3233
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	637
Sbjct	3234	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	3293
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	3294	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	3353
Query	698	GATCTCCTGTTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	3354	GATCTCCTGTTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	3413
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	817
Sbjct	3414	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	3473
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAA	877
Sbjct	3474	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAA	3533
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC	937
Sbjct	3534	GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC	3593
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	997
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Query 998 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
      |||
Sbjct 3654 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 3713

Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 1117
      |||
Sbjct 3714 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 3773

Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
      |||
Sbjct 3774 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 3833

Query 1178 GACGAGTTCTTCTGAG 1193
      |||
Sbjct 3834 GACGAGTTCTTCTGAG 3849
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>gb|EF437950.1| Expression vector pcDNA3-K-AQP4d, complete sequence
Length=6161

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query 398 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGCCCGCTTGGGTGGAGAGGCTATTC 457
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Sbjct 2866 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGCCCGCTTGGGTGGAGAGGCTATTC 2925

Query 458 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
      |||
Sbjct 2926 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 2985

Query 518 GCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577
      |||
Sbjct 2986 GCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 3045

Query 578 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 637
      |||
Sbjct 3046 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 3105

Query 638 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
      |||
Sbjct 3106 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 3165

Query 698 GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
      |||
Sbjct 3166 GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 3225

Query 758 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 817
      |||
Sbjct 3226 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 3285

Query 818 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAA 877
      |||
Sbjct 3286 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAA 3345

Query 878 GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 937
      |||
Sbjct 3346 GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 3405


Query 938 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
      |||
Sbjct 3406 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 3465

Query 998 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
      |||
Sbjct 3466 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 3525

Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 1117
      |||
Sbjct 3526 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 3585

Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
      |||
Sbjct 3586 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 3645

Query 1178 GACGAGTTCTTCTGAG 1193
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Sbjct 3646 GACGAGTTCTTCTGAG 3661
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>gb|CP000744.1|  Pseudomonas aeruginosa PA7, complete genome
Length=6588339

Features in this part of subject sequence:
aminoglycoside 3'-phosphotransferase

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

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Query   398      ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
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Sbjct   3858355  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 385

Query   458      GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          |||
Sbjct   3858295  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 385

Query   518      GCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACCTG 577
          |||
Sbjct   3858235  GCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACCTG 385

Query   578      CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTG 637
          |||
Sbjct   3858175  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTG 385

Query   638      CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
          |||
Sbjct   3858115  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 385

Query   698      GATCTCCTGTCACTACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          |||
Sbjct   3858055  GATCTCCTGTCACTACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 385

Query   758      CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 817
          |||
Sbjct   3857995  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 385

Query   818      ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
          |||
Sbjct   3857935  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 385

Query   878      GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 937
          |||
Sbjct   3857875  GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 385

Query   938      GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT 997
          |||
Sbjct   3857815  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT 385


Query   998      GGCCGCTTTTCTGGATTATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 105
          |||
Sbjct   3857755  GGCCGCTTTTCTGGATTATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 385

Query   1058     ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 111
          |||
Sbjct   3857695  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 385

Query   1118     CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 117
          |||
Sbjct   3857635  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 385

Query   1178     GACGAGTTCTTCTGAG 1193
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Sbjct   3857575  GACGAGTTCTTCTGAG 3857560

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>gb|AY667410.1|  Shuttle cosmid vector pHZ1358, complete sequence
Length=10848

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

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Query   398      ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
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Sbjct  4245  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 4186
Query  458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          |||
Sbjct  4185  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 4126
Query  518    GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT 577
          |||
Sbjct  4125  GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT 4066
Query  578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 637
          |||
Sbjct  4065  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 4006
Query  638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
          |||
Sbjct  4005  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 3946
Query  698    GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          |||
Sbjct  3945  GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 3886
Query  758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 817
          |||
Sbjct  3885  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 3826
Query  818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
          |||
Sbjct  3825  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 3766
Query  878    GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 937
          |||
Sbjct  3765  GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 3706
Query  938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
          |||
Sbjct  3705  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 3646
Query  998    GGCCGCTTTTCTGGATTCAATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          |||
Sbjct  3645  GGCCGCTTTTCTGGATTCAATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 3586
Query  1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 1117
          |||
Sbjct  3585  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 3526
Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||
Sbjct  3525  CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT 3466
Query  1178   GACGAGTTCTTCTGAG 1193
          |||
Sbjct  3465  GACGAGTTCTTCTGAG 3450

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>emb|AM711972.1| Transposon mutagenesis vector pMiET
Length=7819

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query  398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
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Sbjct  6494  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 6553
Query  458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          |||
Sbjct  6554  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 6613
Query  518    GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT 577
          |||
Sbjct  6614  GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT 6673
Query  578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 637
          |||
Sbjct  6674  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 6733
Query  638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
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Sbjct  6734  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 6793
Query  698    GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          |||
Sbjct  6794  GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 6853
Query  758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 817
          |||
Sbjct  6854  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 6913
Query  818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
          |||
Sbjct  6914  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 6973
Query  878    GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 937
          |||
Sbjct  6974  GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 7033
Query  938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT 997
          |||
Sbjct  7034  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT 7093
Query  998    GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          |||
Sbjct  7094  GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 7153
Query  1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 1117
          |||
Sbjct  7154  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 7213
Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||
Sbjct  7214  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 7273
Query  1178   GACGAGTTCTTCTGAG 1193
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Sbjct  7274  GACGAGTTCTTCTGAG 7289

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>gb|EF550208.1| Cloning vector pcDNA3.1+PA, complete sequence
Length=7063

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query  398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
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Sbjct  3771   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 3830
Query  458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          |||
Sbjct  3831   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 3890
Query  518    GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577
          |||
Sbjct  3891   GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 3950
Query  578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 637
          |||
Sbjct  3951   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 4010
Query  638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
          |||
Sbjct  4011   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 4070
Query  698    GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          |||
Sbjct  4071   GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 4130
Query  758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 817
          |||
Sbjct  4131   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 4190
Query  818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
          |||
Sbjct  4191   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 4250
Query  878    GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 937
          |||

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Sbjct  4251  GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC  4310
Query  938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
          |||
Sbjct  4311  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  4370
Query  998    GGCCGCTTTTCTGGATTCAATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
          |||
Sbjct  4371  GGCCGCTTTTCTGGATTCAATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  4430
Query  1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
          |||
Sbjct  4431  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  4490
Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT  1177
          |||
Sbjct  4491  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT  4550
Query  1178   GACGAGTTCTTCTGAG  1193
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Sbjct  4551  GACGAGTTCTTCTGAG  4566
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>gb|EF192606.1|  Cloning vector pBEO210, complete sequence
Length=28953

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query  458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
          |||
Sbjct  16447   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  16506
Query  518    GCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT  577
          |||
Sbjct  16507   GCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT  16566
Query  578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTG  637
          |||
Sbjct  16567   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTG  16626
Query  638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
          |||
Sbjct  16627   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  16686
Query  698    GATCTCCTGTCACTACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
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Sbjct  16687   GATCTCCTGTCACTACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  16746
Query  758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
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Sbjct  16747   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  16806
Query  818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
          |||
Sbjct  16807   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  16866
Query  878    GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC  937
          |||
Sbjct  16867   GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC  16926
Query  938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
          |||
Sbjct  16927   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  16986
Query  998    GGCCGCTTTTCTGGATTCAATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
          |||
Sbjct  16987   GGCCGCTTTTCTGGATTCAATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  17046
Query  1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
          |||
Sbjct  17047   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  17106
Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT  1177
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Sbjct  17107  |||||
CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 17166
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Sbjct  17167  |||||
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>gb|EF028675.1| Cloning vector pDV-NTAP-CYFP, complete sequence
Length=8003

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Sbjct  3062  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 3121
Query  458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
Sbjct  3122  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 3181
Query  518  GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577
Sbjct  3182  GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 3241
Query  578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG 637
Sbjct  3242  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG 3301
Query  638  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
Sbjct  3302  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 3361
Query  698  GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
Sbjct  3362  GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 3421
Query  758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 817
Sbjct  3422  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 3481
Query  818  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
Sbjct  3482  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 3541
Query  878  GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 937
Sbjct  3542  GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 3601
Query  938  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
Sbjct  3602  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 3661
Query  998  GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
Sbjct  3662  GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 3721
Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 1117
Sbjct  3722  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 3781
Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
Sbjct  3782  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 3841
Query  1178  GACGAGTTCTTCTGAG 1193
Sbjct  3842  GACGAGTTCTTCTGAG 3857
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>gb|EF028674.1| Cloning vector pDV-NTAP-CGFP, complete sequence
Length=8003

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query  398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
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Sbjct	3062	 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	3121
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	3122	 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	3181
Query	518	GCGCAGGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	3182	 GCGCAGGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	3241
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	637
Sbjct	3242	 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	3301
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	3302	 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	3361
Query	698	GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	3362	 GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	3421
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	817
Sbjct	3422	 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	3481
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	3482	 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	3541
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC	937
Sbjct	3542	 GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC	3601
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	997
Sbjct	3602	 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	3661
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	3662	 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	3721
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	1117
Sbjct	3722	 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	3781
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	3782	 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	3841
Query	1178	GACGAGTTCTTCTGAG 1193	
Sbjct	3842	 GACGAGTTCTTCTGAG 3857	

>gb|EF028673.1| Cloning vector pDV-CYFP-CTAP, complete sequence
Length=8021

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	3080	 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	3139
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	3140	 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	3199
Query	518	GCGCAGGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	3200	 GCGCAGGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	3259
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	637
Sbjct	3260	 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	3319
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697


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      |||
Sbjct  3320  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 3379
Query  698    GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
      |||
Sbjct  3380  GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 3439
Query  758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 817
      |||
Sbjct  3440  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 3499
Query  818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
      |||
Sbjct  3500  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 3559
Query  878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC 937
      |||
Sbjct  3560  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC 3619
Query  938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAT 997
      |||
Sbjct  3620  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAT 3679
Query  998    GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
      |||
Sbjct  3680  GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 3739
Query  1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 1117
      |||
Sbjct  3740  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 3799
Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
      |||
Sbjct  3800  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 3859
Query  1178   GACGAGTTCTTCTGAG 1193
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Sbjct  3860  GACGAGTTCTTCTGAG 3875

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>gb|EF028672.1| Cloning vector pDV-CGFP-CTAP, complete sequence
Length=8021

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query  398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
      |||
Sbjct  3080  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 3139
Query  458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
      |||
Sbjct  3140  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 3199
Query  518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577
      |||
Sbjct  3200  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 3259
Query  578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG 637
      |||
Sbjct  3260  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG 3319
Query  638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
      |||
Sbjct  3320  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 3379
Query  698    GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
      |||
Sbjct  3380  GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 3439
Query  758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 817
      |||
Sbjct  3440  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 3499
Query  818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
      |||
Sbjct  3500  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 3559
Query  878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC 937

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Sbjct 3560 |||||GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 3619
Query 938 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
Sbjct 3620 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 3679
Query 998 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
Sbjct 3680 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 3739
Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGGCTGACCGCTTC 1117
Sbjct 3740 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGGCTGACCGCTTC 3799
Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
Sbjct 3800 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 3859
Query 1178 GACGAGTTCTTCTGAG 1193
Sbjct 3860 GACGAGTTCTTCTGAG 3875
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>gb|EF028671.1| Cloning vector pDV-NYFP-CTAP, complete sequence
Length=8021

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query 398 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
Sbjct 3080 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 3139
Query 458 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
Sbjct 3140 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 3199
Query 518 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577
Sbjct 3200 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 3259
Query 578 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG 637
Sbjct 3260 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG 3319
Query 638 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
Sbjct 3320 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 3379
Query 698 GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
Sbjct 3380 GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 3439
Query 758 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 817
Sbjct 3440 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 3499
Query 818 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
Sbjct 3500 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 3559
Query 878 GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 937
Sbjct 3560 GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 3619
Query 938 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
Sbjct 3620 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 3679
Query 998 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
Sbjct 3680 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 3739
Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGGCTGACCGCTTC 1117
Sbjct 3740 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGGCTGACCGCTTC 3799
Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
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Sbjct 3800 |CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT| 3859
Query 1178 GACGAGTTCTTCTGAG 1193
          |CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT|
Sbjct 3860 GACGAGTTCTTCTGAG 3875
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>gb|EF028670.1| Cloning vector pDV-NTAP-NYFP, complete sequence
Length=8003

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query 398 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
          |ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC|
Sbjct 3062 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 3121
Query 458 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          |GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA|
Sbjct 3122 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 3181
Query 518 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577
          |GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG|
Sbjct 3182 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 3241
Query 578 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG 637
          |CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG|
Sbjct 3242 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG 3301
Query 638 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
          |CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG|
Sbjct 3302 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 3361
Query 698 GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          |GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG|
Sbjct 3362 GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 3421
Query 758 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 817
          |CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC|
Sbjct 3422 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 3481
Query 818 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
          |ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA|
Sbjct 3482 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 3541
Query 878 GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCGCGCATGCCCCGAC 937
          |GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCGCGCATGCCCCGAC|
Sbjct 3542 GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCGCGCATGCCCCGAC 3601
Query 938 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
          |GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT|
Sbjct 3602 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 3661
Query 998 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          |GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC|
Sbjct 3662 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 3721
Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 1117
          |ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC|
Sbjct 3722 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 3781
Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT|
Sbjct 3782 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 3841
Query 1178 GACGAGTTCTTCTGAG 1193
          |CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT|
Sbjct 3842 GACGAGTTCTTCTGAG 3857
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>gb|EF028669.1| Cloning vector pDV-CTAP, complete sequence
Length=7307

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query 398 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
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Sbjct	2366		ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	2425
Query	458		GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	2426		GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	2485
Query	518		GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	2486		GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	2545
Query	578		CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	637
Sbjct	2546		CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	2605
Query	638		CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	2606		CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	2665
Query	698		GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	2666		GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	2725
Query	758		CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	817
Sbjct	2726		CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	2785
Query	818		ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	2786		ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	2845
Query	878		GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	937
Sbjct	2846		GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	2905
Query	938		GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	997
Sbjct	2906		GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	2965
Query	998		GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	2966		GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	3025
Query	1058		ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	1117
Sbjct	3026		ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	3085
Query	1118		CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	3086		CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	3145
Query	1178		GACGAGTTCTTCTGAG 1193	
Sbjct	3146		GACGAGTTCTTCTGAG 3161	

>gb|EF028668.1| Cloning vector pDV-CYFP, complete sequence
Length=7475

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query	398		ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	2534		ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	2593
Query	458		GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	2594		GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	2653
Query	518		GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	2654		GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	2713
Query	578		CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	637
Sbjct	2714		CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	2773
Query	638		CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697

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      |||
Sbjct  2774  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 2833
      |||
Query  698  GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
      |||
Sbjct  2834  GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 2893
      |||
Query  758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 817
      |||
Sbjct  2894  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 2953
      |||
Query  818  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
      |||
Sbjct  2954  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 3013
      |||
Query  878  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC 937
      |||
Sbjct  3014  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC 3073
      |||
Query  938  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAT 997
      |||
Sbjct  3074  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAT 3133
      |||
Query  998  GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
      |||
Sbjct  3134  GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 3193
      |||
Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 1117
      |||
Sbjct  3194  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 3253
      |||
Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
      |||
Sbjct  3254  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 3313
      |||
Query  1178  GACGAGTTCTTCTGAG 1193
      |||
Sbjct  3314  GACGAGTTCTTCTGAG 3329

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>gb|EF028667.1| Cloning vector pDV-CGFP, complete sequence
Length=7475

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query  398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
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Sbjct  2534  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 2593
      |||
Query  458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
      |||
Sbjct  2594  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 2653
      |||
Query  518  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577
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Sbjct  2654  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 2713
      |||
Query  578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG 637
      |||
Sbjct  2714  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG 2773
      |||
Query  638  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
      |||
Sbjct  2774  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 2833
      |||
Query  698  GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
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Sbjct  2834  GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 2893
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Query  758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 817
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Sbjct  2894  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 2953
      |||
Query  818  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
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Sbjct  2954  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 3013
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Query  878  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC 937

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Sbjct 3014 |||||GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 3073
Query 938 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
Sbjct 3074 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 3133
Query 998 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
Sbjct 3134 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 3193
Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 1117
Sbjct 3194 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 3253
Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
Sbjct 3254 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 3313
Query 1178 GACGAGTTCTTCTGAG 1193
Sbjct 3314 GACGAGTTCTTCTGAG 3329
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>gb|EF028666.1| Cloning vector pDV-NTAP, complete sequence
Length=7289

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Sbjct 2348 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 2407
Query 458 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
Sbjct 2408 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 2467
Query 518 GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577
Sbjct 2468 GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 2527
Query 578 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG 637
Sbjct 2528 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG 2587
Query 638 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
Sbjct 2588 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 2647
Query 698 GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
Sbjct 2648 GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 2707
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Sbjct 2708 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 2767
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Sbjct 2768 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 2827
Query 878 GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 937
Sbjct 2828 GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 2887
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Sbjct 2888 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 2947
Query 998 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
Sbjct 2948 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 3007
Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 1117
Sbjct 3008 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 3067
Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
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Sbjct  3068  |||||
CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGACGCGCATCGCCTTCTATCGCCTTCTT 3127
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>gb|EF028665.1| Cloning vector pDV-NYFP, complete sequence
Length=7475

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Sbjct  2534  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 2593
Query  458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
|||
Sbjct  2594  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 2653
Query  518  GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577
|||
Sbjct  2654  GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 2713
Query  578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG 637
|||
Sbjct  2714  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG 2773
Query  638  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
|||
Sbjct  2774  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 2833
Query  698  GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
|||
Sbjct  2834  GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 2893
Query  758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 817
|||
Sbjct  2894  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 2953
Query  818  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
|||
Sbjct  2954  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 3013
Query  878  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCGCGCATGCCCGAC 937
|||
Sbjct  3014  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCGCGCATGCCCGAC 3073
Query  938  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
|||
Sbjct  3074  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 3133
Query  998  GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
|||
Sbjct  3134  GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 3193
Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 1117
|||
Sbjct  3194  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 3253
Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGACGCGCATCGCCTTCTATCGCCTTCTT 1177
|||
Sbjct  3254  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGACGCGCATCGCCTTCTATCGCCTTCTT 3313
Query  1178  GACGAGTTCTTCTGAG  1193
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Sbjct  3314  GACGAGTTCTTCTGAG  3329
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>gb|EF028664.1| Cloning vector EXP5(+), complete sequence
Length=6761

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query  398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
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Sbjct	1820		ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	1879
Query	458		GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	1880		GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	1939
Query	518		GCGCAGGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	1940		GCGCAGGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	1999
Query	578		CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	637
Sbjct	2000		CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	2059
Query	638		CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	2060		CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	2119
Query	698		GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	2120		GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	2179
Query	758		CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	817
Sbjct	2180		CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	2239
Query	818		ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	2240		ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	2299
Query	878		GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	937
Sbjct	2300		GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	2359
Query	938		GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT	997
Sbjct	2360		GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT	2419
Query	998		GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	2420		GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	2479
Query	1058		ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	1117
Sbjct	2480		ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	2539
Query	1118		CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	2540		CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	2599
Query	1178		GACGAGTTCTTCTGAG 1193	
Sbjct	2600		GACGAGTTCTTCTGAG 2615	

>gb|EF028663.1| Cloning vector EXP4(+), complete sequence
Length=6724

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query	398		ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	1791		ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	1850
Query	458		GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	1851		GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	1910
Query	518		GCGCAGGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	1911		GCGCAGGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	1970
Query	578		CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	637
Sbjct	1971		CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	2030
Query	638		CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697

Sbjct	2031	 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	2090
Query	698	GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	2091	 GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	2150
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	817
Sbjct	2151	 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	2210
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	2211	 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	2270
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC	937
Sbjct	2271	 GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC	2330
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	997
Sbjct	2331	 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	2390
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	2391	 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	2450
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	1117
Sbjct	2451	 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	2510
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	2511	 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	2570
Query	1178	GACGAGTTCTTCTGAG 1193	
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>gb|EF177812.1| Expression vector pUNIV, complete sequence
Length=5653

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	2644	 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	2703
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	2704	 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	2763
Query	518	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	2764	 GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	2823
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	637
Sbjct	2824	 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	2883
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	2884	 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	2943
Query	698	GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	2944	 GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	3003
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	817
Sbjct	3004	 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	3063
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	3064	 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	3123
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC	937

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Sbjct 3124 |||||GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 3183
Query 938 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
Sbjct 3184 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 3243
Query 998 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
Sbjct 3244 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 3303
Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 1117
Sbjct 3304 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 3363
Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
Sbjct 3364 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 3423
Query 1178 GACGAGTTCTTCTGAG 1193
Sbjct 3424 GACGAGTTCTTCTGAG 3439
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>gb|EF030522.1| Inducible protein expression vector pReg Neo, complete sequence
Length=6802

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query 398 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
Sbjct 3793 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 3852
Query 458 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
Sbjct 3853 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 3912
Query 518 GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577
Sbjct 3913 GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 3972
Query 578 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG 637
Sbjct 3973 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG 4032
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Sbjct 4033 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 4092
Query 698 GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
Sbjct 4093 GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 4152
Query 758 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 817
Sbjct 4153 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 4212
Query 818 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
Sbjct 4213 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 4272
Query 878 GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 937
Sbjct 4273 GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 4332
Query 938 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
Sbjct 4333 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 4392
Query 998 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
Sbjct 4393 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 4452
Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 1117
Sbjct 4453 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 4512
Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
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Sbjct  4513  |||||
CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGCAGCGCATCGCCTTCTATCGCCTTCTT  4572
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Sbjct  4573  |||||
GACGAGTTCTTCTGAG  4588
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>dbj|AB255435.1|  Escherichia coli plasmid pO86A1 DNA, complete sequence
Length=120730

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query  398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
Sbjct  116462 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  1165
Query  458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
Sbjct  116522 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  1165
Query  518  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
Sbjct  116582 GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  1166
Query  578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCAGCTGTG  637
Sbjct  116642 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCAGCTGTG  1167
Query  638  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
Sbjct  116702 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  1167
Query  698  GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
Sbjct  116762 GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  1168
Query  758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC  817
Sbjct  116822 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC  1168
Query  818  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAA  877
Sbjct  116882 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAA  1169
Query  878  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC  937
Sbjct  116942 GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC  1170
Query  938  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT  997
Sbjct  117002 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT  1170
Query  998  GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
Sbjct  117062 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1171
Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
Sbjct  117122 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1171
Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
Sbjct  117182 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1172
Query  1178  GACGAGTTCTTCTGAG  1193
Sbjct  117242 GACGAGTTCTTCTGAG  117257
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>gb|DQ886588.1| Expression vector pcDNA3-hFIX, complete sequence
Length=8223

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus


Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	4928	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	4987
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	4988	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	5047
Query	518	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	5048	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	5107
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	637
Sbjct	5108	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	5167
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	5168	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	5227
Query	698	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	5228	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	5287
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	817
Sbjct	5288	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	5347
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	5348	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	5407
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC	937
Sbjct	5408	GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC	5467
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	997
Sbjct	5468	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	5527
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	5528	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	5587
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	1117
Sbjct	5588	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	5647
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	5648	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	5707
Query	1178	GACGAGTTCTTCTGAG	1193
Sbjct	5708	GACGAGTTCTTCTGAG	5723

>gb|DQ898181.1| Keratinocyte expression vector phPK14H, complete sequence
Length=6815

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	3520	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	3579
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	3580	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	3639
Query	518	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	3640	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	3699
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	637
Sbjct	3700	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	3759

Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	3760	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	3819
Query	698	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	3820	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	3879
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	817
Sbjct	3880	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	3939
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	3940	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	3999
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	937
Sbjct	4000	GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	4059
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	997
Sbjct	4060	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	4119
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	4120	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	4179
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	1117
Sbjct	4180	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	4239
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	4240	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	4299
Query	1178	GACGAGTTCTTCTGAG	1193
Sbjct	4300	GACGAGTTCTTCTGAG	4315

>gb|DQ823233.1|  Expression vector mce4, complete sequence
Length=29048

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	25966	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	26025
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	26026	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	26085
Query	518	GCGCAGGGGCGCCCGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	26086	GCGCAGGGGCGCCCGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	26145
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTG	637
Sbjct	26146	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTG	26205
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	26206	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	26265
Query	698	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	26266	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	26325
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	817
Sbjct	26326	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	26385
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	26386	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	26445

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Query 878 GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 937
          |||
Sbjct 26446 GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 26505


Query 938 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT 997
          |||
Sbjct 26506 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT 26565

Query 998 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          |||
Sbjct 26566 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 26625

Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGGCTGACCGCTTC 1117
          |||
Sbjct 26626 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGGCTGACCGCTTC 26685

Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||
Sbjct 26686 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 26745

Query 1178 GACGAGTTCTTCTGAG 1193
          |||
Sbjct 26746 GACGAGTTCTTCTGAG 26761
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>gb|DQ823232.1|  Expression vector mce3, complete sequence
Length=38473

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query 398 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
          |||
Sbjct 35391 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 35450

Query 458 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          |||
Sbjct 35451 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 35510

Query 518 GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577
          |||
Sbjct 35511 GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 35570

Query 578 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTG 637
          |||
Sbjct 35571 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTG 35630

Query 638 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
          |||
Sbjct 35631 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 35690

Query 698 GATCTCCTGTCTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          |||
Sbjct 35691 GATCTCCTGTCTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 35750

Query 758 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 817
          |||
Sbjct 35751 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 35810

Query 818 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
          |||
Sbjct 35811 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 35870


Query 878 GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 937
          |||
Sbjct 35871 GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 35930

Query 938 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT 997
          |||
Sbjct 35931 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT 35990

Query 998 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          |||
Sbjct 35991 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 36050

Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGGCTGACCGCTTC 1117
          |||
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Sbjct  36051  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 36110
Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||
Sbjct  36111  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 36170
Query  1178   GACGAGTTCTTCTGAG 1193
          |||
Sbjct  36171  GACGAGTTCTTCTGAG 36186
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>gb|DQ823231.1|  Expression vector mce2, complete sequence
Length=24799

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query  398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
          |||
Sbjct  21717  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 21776
Query  458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          |||
Sbjct  21777  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 21836
Query  518   GCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAC TG 577
          |||
Sbjct  21837  GCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAC TG 21896
Query  578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTG 637
          |||
Sbjct  21897  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTG 21956
Query  638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
          |||
Sbjct  21957  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 22016
Query  698   GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          |||
Sbjct  22017  GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 22076
Query  758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 817
          |||
Sbjct  22077  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 22136
Query  818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
          |||
Sbjct  22137  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 22196
Query  878   GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 937
          |||
Sbjct  22197  GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 22256
Query  938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT 997
          |||
Sbjct  22257  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT 22316
Query  998   GGCCGCTTTTCTGGATTATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          |||
Sbjct  22317  GGCCGCTTTTCTGGATTATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 22376
Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 1117
          |||
Sbjct  22377  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 22436
Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||
Sbjct  22437  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 22496
Query  1178  GACGAGTTCTTCTGAG 1193
          |||
Sbjct  22497  GACGAGTTCTTCTGAG 22512
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>gb|DQ487156.1| Flexi vector pF5K CMV-neo, complete sequence
Length=4594

Score = 1471 bits (796), Expect = 0.0

Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	2409	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	2468
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	2469	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	2528
Query	518	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	2529	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	2588
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	637
Sbjct	2589	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	2648
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	2649	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	2708
Query	698	GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	2709	GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	2768
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	817
Sbjct	2769	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	2828
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	2829	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	2888
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTTCGCCAGGCTCAAGGCGCGCATGCCCGAC	937
Sbjct	2889	GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTTCGCCAGGCTCAAGGCGCGCATGCCCGAC	2948
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	997
Sbjct	2949	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	3008
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	3009	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	3068
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	1117
Sbjct	3069	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	3128
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	3129	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	3188
Query	1178	GACGAGTTCTTCTGAG 1193	
Sbjct	3189	GACGAGTTCTTCTGAG 3204	

>gb|DQ487155.1| Flexi vector pF5A CMV-neo, complete sequence
Length=5591

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	2366	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	2425
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	2426	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	2485
Query	518	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	2486	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	2545
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	637

Sbjct	2546	 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	2605
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	2606	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	2665
Query	698	GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	2666	GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	2725
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	817
Sbjct	2726	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	2785
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	2786	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	2845
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC	937
Sbjct	2846	GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC	2905
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	997
Sbjct	2906	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	2965
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	2966	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	3025
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	1117
Sbjct	3026	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	3085
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	3086	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	3145
Query	1178	GACGAGTTCTTCTGAG 1193	
Sbjct	3146	 GACGAGTTCTTCTGAG 3161	

>gb|DQ487211.1| Flexi Vector pFN10A (ACT), complete sequence
Length=5867

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	2642	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	2701
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	2702	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	2761
Query	518	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	2762	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	2821
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	637
Sbjct	2822	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	2881
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	2882	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	2941
Query	698	GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	2942	GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	3001
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	817
Sbjct	3002	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	3061
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877

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Sbjct  3062  |||||
ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAA 3121
Query  878  GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 937
Sbjct  3122  GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 3181
Query  938  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
Sbjct  3182  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 3241
Query  998  GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
Sbjct  3242  GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 3301
Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGGCTGACCGCTTC 1117
Sbjct  3302  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGGCTGACCGCTTC 3361
Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
Sbjct  3362  CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT 3421
Query  1178  GACGAGTTCTTCTGAG 1193
Sbjct  3422  GACGAGTTCTTCTGAG 3437
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>gb|DQ515893.1| HIS3/URA3 reporter vector pH3U3, complete sequence
Length=5834

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

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Query  398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
Sbjct  3264  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 3205
Query  458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
Sbjct  3204  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 3145
Query  518  GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577
Sbjct  3144  GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 3085
Query  578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG 637
Sbjct  3084  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG 3025
Query  638  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
Sbjct  3024  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 2965
Query  698  GATCTCCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
Sbjct  2964  GATCTCCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 2905
Query  758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 817
Sbjct  2904  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 2845
Query  818  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAA 877
Sbjct  2844  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAA 2785
Query  878  GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 937
Sbjct  2784  GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 2725
Query  938  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
Sbjct  2724  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 2665
Query  998  GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
Sbjct  2664  GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 2605
Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGGCTGACCGCTTC 1117
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11/17/2008

Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

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Query   398      ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
          |||
Sbjct   14079     ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 14020

Query   458      GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          |||
Sbjct   14019     GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 13960

Query   518      GCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT 577
          |||
Sbjct   13959     GCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT 13900

Query   578      CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTG 637
          |||
Sbjct   13899     CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTG 13840

Query   638      CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
          |||
Sbjct   13839     CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 13780

Query   698      GATCTCCTGTCTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          |||
Sbjct   13779     GATCTCCTGTCTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 13720

Query   758      CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 817
          |||
Sbjct   13719     CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 13660

Query   818      ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
          |||
Sbjct   13659     ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 13600

Query   878      GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 937
          |||
Sbjct   13599     GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 13540


Query   938      GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT 997
          |||
Sbjct   13539     GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT 13480

Query   998      GGCCGCTTTTCTGGATTATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          |||
Sbjct   13479     GGCCGCTTTTCTGGATTATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 13420

Query   1058     ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 1117
          |||
Sbjct   13419     ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 13360

Query   1118     CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||
Sbjct   13359     CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 13300

Query   1178     GACGAGTTCTTCTGAG 1193
          |||
Sbjct   13299     GACGAGTTCTTCTGAG 13284
  
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>gb|AY266291.1|  Escherichia coli/Mycobacteria shuttle vector pGB9.2, complete sequence
 Length=11441

Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query   398      ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
          |||
Sbjct   334      ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 393

Query   458      GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          |||
Sbjct   394      GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 453

Query   518      GCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT 577
          |||
  
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Sbjct  454      GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG      513
Query  578      CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG      637
          |||
Sbjct  514      CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG      573
Query  638      CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG      697
          |||
Sbjct  574      CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG      633
Query  698      GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG      757
          |||
Sbjct  634      GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG      693
Query  758      CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC      817
          |||
Sbjct  694      CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC      753
Query  818      ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA      877
          |||
Sbjct  754      ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA      813
Query  878      GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC      937
          |||
Sbjct  814      GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC      873
Query  938      GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT      997
          |||
Sbjct  874      GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT      933
Query  998      GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC      1057
          |||
Sbjct  934      GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC      993
Query  1058     ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC      1117
          |||
Sbjct  994      ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC      1053
Query  1118     CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT      1177
          |||
Sbjct  1054     CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT      1113
Query  1178     GACGAGTTCTTCTGAG      1193
          |||
Sbjct  1114     GACGAGTTCTTCTGAG      1129

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>gb|AY613997.1| Cloning vector pSRalphaneor, complete sequence
Length=6423

Sort alignments for this
E value Score Percen
Query start position

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

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Query  398      ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC      457
          |||
Sbjct  3088     ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC      3029
Query  458      GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA      517
          |||
Sbjct  3028     GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA      2969
Query  518      GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG      577
          |||
Sbjct  2968     GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG      2909
Query  578      CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG      637
          |||
Sbjct  2908     CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG      2849
Query  638      CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG      697
          |||
Sbjct  2848     CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG      2789
Query  698      GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG      757
          |||

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Sbjct	2788	GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	2729
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	817
Sbjct	2728	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	2669
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	2668	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	2609
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC	937
Sbjct	2608	GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC	2549
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	997
Sbjct	2548	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	2489
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	2488	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	2429
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	1117
Sbjct	2428	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	2369
Query	1118	CTCGTGTCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	2368	CTCGTGTCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	2309
Query	1178	GACGAGTTCTTCTGAG	1193
Sbjct	2308	GACGAGTTCTTCTGAG	2293

Score = 1057 bits (572), Expect = 0.0
 Identities = 572/572 (100%), Gaps = 0/572 (0%)
 Strand=Plus/Plus

Query	1200	CCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGAATAAGGCCGGTGT	1259
Sbjct	101	CCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGAATAAGGCCGGTGT	160
Query	1260	GCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGG	1319
Sbjct	161	GCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGG	220
Query	1320	AAACCTGGCCCTGTCTTCTTGACGAGCATTCTAGGGGTCTTTCCCTCTCGCCAAAGGA	1379
Sbjct	221	AAACCTGGCCCTGTCTTCTTGACGAGCATTCTAGGGGTCTTTCCCTCTCGCCAAAGGA	280
Query	1380	ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA	1439
Sbjct	281	ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA	340
Query	1440	ACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCACCTGGCGACAGGTGCCTC	1499
Sbjct	341	ACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCACCTGGCGACAGGTGCCTC	400
Query	1500	TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCAGTGCCAC	1559
Sbjct	401	TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCAGTGCCAC	460
Query	1560	GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG	1619
Sbjct	461	GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG	520
Query	1620	GGGCTGAAGGATGCCCAGAAGGTACCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC	1679
Sbjct	521	GGGCTGAAGGATGCCCAGAAGGTACCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC	580
Query	1680	ACATGCTTTTACATGTGTTTAGTCGAGGTTAAAAAAGCGTCTAGGCCCCCGAACCACGGG	1739
Sbjct	581	ACATGCTTTTACATGTGTTTAGTCGAGGTTAAAAAAGCGTCTAGGCCCCCGAACCACGGG	640
Query	1740	GACGTGGTTTTCTTTGAAAAACACGATGATA	1771
Sbjct	641	GACGTGGTTTTCTTTGAAAAACACGATGATA	672

Score = 1057 bits (572), Expect = 0.0
 Identities = 572/572 (100%), Gaps = 0/572 (0%)
 Strand=Plus/Plus

Query	1200	CCCTCTCCCT	1259
Sbjct	787	CCCTCTCCCT	846
Query	1260	GCGTTTGTCTATATGTTATTTTCACCATATTGCCGTC	1319
Sbjct	847	GCGTTTGTCTATATGTTATTTTCACCATATTGCCGTC	906
Query	1320	AAACCTGGCCCTGTCTTCTTGACGAGCATTCTAGGGGTCTTCCCTCTCGCCAAAGGA	1379
Sbjct	907	AAACCTGGCCCTGTCTTCTTGACGAGCATTCTAGGGGTCTTCCCTCTCGCCAAAGGA	966
Query	1380	ATGCAAGGTCGTGTAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA	1439
Sbjct	967	ATGCAAGGTCGTGTAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA	1026
Query	1440	ACAACGTCGTAGCGACCCCTTTCAGGCAGCGGAACCCCCACCTGGCGACAGGTGCCTC	1499
Sbjct	1027	ACAACGTCGTAGCGACCCCTTTCAGGCAGCGGAACCCCCACCTGGCGACAGGTGCCTC	1086
Query	1500	TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCAGTGCCAC	1559
Sbjct	1087	TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCAGTGCCAC	1146
Query	1560	GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG	1619
Sbjct	1147	GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG	1206
Query	1620	GGGCTGAAGGATGCCCAGAAGGTACCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC	1679
Sbjct	1207	GGGCTGAAGGATGCCCAGAAGGTACCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC	1266
Query	1680	ACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAGCTCTAGGCCCCCGAACCACGGG	1739
Sbjct	1267	ACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAGCTCTAGGCCCCCGAACCACGGG	1326
Query	1740	GACGTGGTTTTCTTTGAAAAACACGATGATA	1771
Sbjct	1327	GACGTGGTTTTCTTTGAAAAACACGATGATA	1358

>gb|AY613992.1| Cloning vector pSRalphaneo, complete sequence
 Length=4542

Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTC	457
Sbjct	1207	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTC	1148
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	1147	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	1088
Query	518	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	1087	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	1028
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	637
Sbjct	1027	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	968
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	967	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	908
Query	698	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	907	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	848
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	817
Sbjct	847	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	788

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Query 818 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
      |||
Sbjct 787 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 728

Query 878 GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC 937
      |||
Sbjct 727 GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC 668

Query 938 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
      |||
Sbjct 667 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 608

Query 998 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
      |||
Sbjct 607 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 548

Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 1117
      |||
Sbjct 547 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 488

Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
      |||
Sbjct 487 CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT 428

Query 1178 GACGAGTTCTTCTGAG 1193
      |||
Sbjct 427 GACGAGTTCTTCTGAG 412
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>gb|AY286001.1| Cloning vector pHRE1-km, complete sequence
Length=9037

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

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Query 398 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
      |||
Sbjct 3776 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 3717

Query 458 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
      |||
Sbjct 3716 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 3657

Query 518 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577
      |||
Sbjct 3656 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 3597

Query 578 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 637
      |||
Sbjct 3596 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 3537

Query 638 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
      |||
Sbjct 3536 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 3477

Query 698 GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
      |||
Sbjct 3476 GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 3417

Query 758 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACACCAAGCGAAACATCGC 817
      |||
Sbjct 3416 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACACCAAGCGAAACATCGC 3357

Query 818 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
      |||
Sbjct 3356 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 3297

Query 878 GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC 937
      |||
Sbjct 3296 GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC 3237

Query 938 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
      |||
Sbjct 3236 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 3177


Query 998 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
      |||
Sbjct 3176 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 3117
```



```
Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 1117
          |||
Sbjct 3116 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 3057

Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||
Sbjct 3056 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 2997

Query 1178 GACGAGTTCTTCTGAG 1193
          |||
Sbjct 2996 GACGAGTTCTTCTGAG 2981
```

>gb|DQ059989.1|  Cloning vector pSCR001, complete sequence
Length=10571

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query 398 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGCCGCTTGGGTGGAGAGGCTATTC 457
          |||
Sbjct 7019 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGCCGCTTGGGTGGAGAGGCTATTC 7078

Query 458 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          |||
Sbjct 7079 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 7138

Query 518 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577
          |||
Sbjct 7139 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 7198

Query 578 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 637
          |||
Sbjct 7199 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 7258

Query 638 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
          |||
Sbjct 7259 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 7318

Query 698 GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          |||
Sbjct 7319 GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 7378

Query 758 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 817
          |||
Sbjct 7379 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 7438

Query 818 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
          |||
Sbjct 7439 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 7498

Query 878 GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC 937
          |||
Sbjct 7499 GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC 7558

Query 938 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
          |||
Sbjct 7559 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 7618

Query 998 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          |||
Sbjct 7619 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 7678

Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 1117
          |||
Sbjct 7679 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 7738

Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||
Sbjct 7739 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 7798

Query 1178 GACGAGTTCTTCTGAG 1193
          |||
Sbjct 7799 GACGAGTTCTTCTGAG 7814
```

>gb|AY260554.1| Retrotransposon vector MEL/ELM, complete sequence
Length=9945

Sort alignments for this
E value Score Perce
Query start position

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	5600	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	5659
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	5660	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	5719
Query	518	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	5720	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	5779
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	637
Sbjct	5780	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	5839
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	5840	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	5899
Query	698	GATCTCCTGTCACTCTACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	5900	GATCTCCTGTCACTCTACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	5959
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCACCAAGCGAAACATCGC	817
Sbjct	5960	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCACCAAGCGAAACATCGC	6019
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	6020	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	6079
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC	937
Sbjct	6080	GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC	6139
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	997
Sbjct	6140	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	6199
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	6200	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	6259
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	1117
Sbjct	6260	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	6319
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	6320	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	6379
Query	1178	GACGAGTTCTTCTGAG 1193	
Sbjct	6380	GACGAGTTCTTCTGAG 6395	

Score = 1024 bits (554), Expect = 0.0
Identities = 559/561 (99%), Gaps = 1/561 (0%)
Strand=Plus/Plus

Query	1211	ccccccccTAACGTTACTGGCCGAAGCCGCTTGAATAAGGCCGGTGTGCGTTTGTCTA	1270
Sbjct	1249	CCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGAATAAGGCCGGTGTGCGTTTGTCTA	1308
Query	1271	TATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCC	1330
Sbjct	1309	TATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCC	1368
Query	1331	TGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCT	1390

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Sbjct 1369 TGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCT 1428
Query 1391 GTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGT 1450
          |||
Sbjct 1429 GTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGT 1488
Query 1451 AGCGACCCCTTTGCAGGCAGCGGAACCCCCACCTGGCGACAGGTGCCTCTGCGGCCAAAA 1510
          |||
Sbjct 1489 AGCGACCCCTTTGCAGGCAGCGGAACCCCCACCTGGCGACAGGTGCCTCTGCGGCCAAAA 1548
Query 1511 GCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTG 1570
          |||
Sbjct 1549 GCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTG 1608
Query 1571 GATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGA 1630
          |||
Sbjct 1609 GATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGA 1668
Query 1631 TGCCCAGAAGGTACCCCATTTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTAC 1690
          |||
Sbjct 1669 TGCCCAGAAGGTACCCCATTTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTAC 1728
Query 1691 ATGTGTTTAGTCGAGGTT*****CGTCTAGGCCCCCCGAACCACGGGGACGTGGTTTT 1750
          |||
Sbjct 1729 ATGTGTTTAGTCGAGGTTAAAAAA-CGTCTAGGCCCCCCGAACCACGGGGACGTGGTTTT 1787
Query 1751 CCTTTGAAAAACACGATGATA 1771
          |||
Sbjct 1788 CCTTTGAAAAACACGATAATA 1808
```

>gb|AY260553.1|  Retrotransposon vector ELM 5, complete sequence
Length=10047

Sort alignments for this
E value Score Percen
Query start position

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query 398 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
          |||
Sbjct 5651 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 5710
Query 458 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          |||
Sbjct 5711 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 5770
Query 518 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAC TG 577
          |||
Sbjct 5771 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAC TG 5830
Query 578 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 637
          |||
Sbjct 5831 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 5890
Query 638 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
          |||
Sbjct 5891 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 5950
Query 698 GATCTCCTGTCACTCTACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          |||
Sbjct 5951 GATCTCCTGTCACTCTACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 6010
Query 758 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 817
          |||
Sbjct 6011 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 6070
Query 818 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
          |||
Sbjct 6071 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 6130
Query 878 GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC 937
          |||
Sbjct 6131 GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC 6190
Query 938 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT 997
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Score = 1024 bits (554), Expect = 0.0
Identities = 559/561 (99%), Gaps = 1/561 (0%)
Strand=Plus/Plus

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>gb|AY037297.1| Synthetic construct erythromycin resistance protein (erm) gene,
partial cds; and streptomycin 3'-phosphotransferase (sph),
bleomycin phosphotransferase (ble), neomycin phosphotransferase
(nptII), and gentamycin resistance protein (aac) genes,
complete cds
Length=7080
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Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTGGGTGGAGAGGCTATTC	457
Spict	4740	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTGGGTGGAGAGGCTATTC	4681

Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	4680	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	4621
Query	518	GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	4620	GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	4561
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	637
Sbjct	4560	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	4501
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	4500	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	4441
Query	698	GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	4440	GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	4381
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	817
Sbjct	4380	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	4321
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	4320	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	4261
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	937
Sbjct	4260	GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	4201
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT	997
Sbjct	4200	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT	4141
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	4140	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	4081
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	1117
Sbjct	4080	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	4021
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	4020	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	3961
Query	1178	GACGAGTTCTTCTGAG	1193
Sbjct	3960	GACGAGTTCTTCTGAG	3945

>gb|AF264696.2|  Cloning vector pFB-ERV, complete sequence
Length=11065

Sort alignments for this
E value Score Percen
Query start position

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTC	457
Sbjct	7575	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTC	7634
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	7635	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	7694
Query	518	GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	7695	GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	7754
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	637
Sbjct	7755	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	7814

Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	7815	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	7874
Query	698	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	7875	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	7934
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCACCAAGCGAAACATCGC	817
Sbjct	7935	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCACCAAGCGAAACATCGC	7994
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	7995	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	8054
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC	937
Sbjct	8055	GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC	8114
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	997
Sbjct	8115	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	8174
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	8175	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	8234
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	1117
Sbjct	8235	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	8294
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	8295	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	8354
Query	1178	GACGAGTTCTTCTGAG 1193	
Sbjct	8355	GACGAGTTCTTCTGAG 8370	

Score = 1046 bits (566), Expect = 0.0
 Identities = 571/573 (99%), Gaps = 2/573 (0%)
 Strand=Plus/Plus

Query	1200	CCCTCTCCCTTCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGT	1259
Sbjct	4968	CCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGT	5027
Query	1260	GCGTTTGTCTATATGTTATTTTCCACCATATTGCCGCTTTTGGCAATGTGAGGGCCCGG	1319
Sbjct	5028	GCGTTTGTCTATATGTTATTTTCCACCATATTGCCGCTTTTGGCAATGTGAGGGCCCGG	5087
Query	1320	AAACCTGGCCCTGTCTTCTTGACGAGCATTCTAGGGGTCTTTCCCTCTCGCCAAAGGA	1379
Sbjct	5088	AAACCTGGCCCTGTCTTCTTGACGAGCATTCTAGGGGTCTTTCCCTCTCGCCAAAGGA	5147
Query	1380	ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA	1439
Sbjct	5148	ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA	5207
Query	1440	ACAACGTCTGTAGCGACCCCTTTCAGGCAGCGGAACCCCCACCTGGCGACAGGTGCCTC	1499
Sbjct	5208	ACAACGTCTGTAGCGACCCCTTTCAGGCAGCGGAACCCCCACCTGGCGACAGGTGCCTC	5267
Query	1500	TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCAGTGCCAC	1559
Sbjct	5268	TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCAGTGCCAC	5327
Query	1560	GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG	1619
Sbjct	5328	GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG	5387
Query	1620	GGGCTGAAGGATGCCCAGAAGGTACCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC	1679
Sbjct	5388	GGGCTGAAGGATGCCCAGAAGGTACCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC	5447
Query	1680	ACATGCTTTTACATGTGTTTAGTCGAGGTTAAAAAAGCTCTAGGCCCCCGAACCACGGG	1739

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Sbjct  5448  ACATGCTTTACATGTGTTTAGTCGAGGTTAAAAA-CGTCTAGGCCCCCGAACCACGGG  5506
Query   1740  GACGTGGTTTTTCCTTTGAAAAACACGAT-GATA  1771
          |||||
Sbjct  5507  GACGTGGTTTTTCCTTTGAAAAACACGATCGATA  5539

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Score = 913 bits (494), Expect = 0.0
 Identities = 497/498 (99%), Gaps = 1/498 (0%)
 Strand=Plus/Plus

```

Query   1274  GTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGT  1333
          |||||
Sbjct   6975  GTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGT  7034
Query   1334  CTTCTTGACGAGCATTTCCTAGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTT  1393
          |||||
Sbjct   7035  CTTCTTGACGAGCATTTCCTAGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTT  7094
Query   1394  GAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAGC  1453
          |||||
Sbjct   7095  GAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAGC  7154
Query   1454  GACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCC  1513
          |||||
Sbjct   7155  GACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCC  7214
Query   1514  ACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCAGTGCCACGTTGTGAGTTGGAT  1573
          |||||
Sbjct   7215  ACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCAGTGCCACGTTGTGAGTTGGAT  7274
Query   1574  AGTTGTGGAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGC  1633
          |||||
Sbjct   7275  AGTTGTGGAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGC  7334
Query   1634  CCAGAAGGTACCCCATTTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTACATG  1693
          |||||
Sbjct   7335  CCAGAAGGTACCCCATTTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTACATG  7394
Query   1694  TGTTTAGTCGAGGTTAAAAAAGCGTCTAGGCCCCCGAACCACGGGGACGTGGTTTTTCCT  1753
          |||||
Sbjct   7395  TGTTTAGTCGAGGTTAAAAA-CGTCTAGGCCCCCGAACCACGGGGACGTGGTTTTTCCT  7453
Query   1754  TTGAAAAACACGATGATA  1771
          |||||
Sbjct   7454  TTGAAAAACACGATGATA  7471

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>gb|DQ092437.1|  Insertion vector pWSMK-T, complete sequence
 Length=15969

Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query   398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
          |||||
Sbjct   7376  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  7435
Query   458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
          |||||
Sbjct   7436  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  7495
Query   518  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
          |||||
Sbjct   7496  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  7555
Query   578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
          |||||
Sbjct   7556  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  7615
Query   638  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
          |||||
Sbjct   7616  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  7675
Query   698  GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
          |||||
Sbjct   7676  GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  7735

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Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	817
Sbjct	7736	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	7795
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	7796	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	7855
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC	937
Sbjct	7856	GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC	7915
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	997
Sbjct	7916	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	7975
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	7976	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	8035
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	1117
Sbjct	8036	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	8095
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	8096	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	8155
Query	1178	GACGAGTTCTTCTGAG	1193
Sbjct	8156	GACGAGTTCTTCTGAG	8171

>gb|AF504908.1| Cloning vector pBBRT, complete sequence
Length=5973

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTC	457
Sbjct	4687	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTC	4628
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	4627	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	4568
Query	518	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACCTG	577
Sbjct	4567	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACCTG	4508
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	637
Sbjct	4507	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	4448
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	4447	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	4388
Query	698	GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	4387	GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	4328
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	817
Sbjct	4327	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	4268
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	4267	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	4208
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC	937
Sbjct	4207	GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCCGAC	4148
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	997
Sbjct	4147	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	4088


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Query 998   GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          |||
Sbjct 4087   GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 4028

Query 1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 1117
          |||
Sbjct 4027   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 3968

Query 1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||
Sbjct 3967   CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 3908

Query 1178   GACGAGTTCTTCTGAG 1193
          |||
Sbjct 3907   GACGAGTTCTTCTGAG 3892
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>gb|AY062236.1| Transformation vector pRLE6, complete sequence
Length=5844

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query 398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
          |||
Sbjct 366   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 425

Query 458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          |||
Sbjct 426   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 485

Query 518   GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT 577
          |||
Sbjct 486   GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT 545

Query 578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 637
          |||
Sbjct 546   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 605

Query 638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
          |||
Sbjct 606   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 665

Query 698   GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          |||
Sbjct 666   GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 725

Query 758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 817
          |||
Sbjct 726   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 785

Query 818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
          |||
Sbjct 786   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 845

Query 878   GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 937
          |||
Sbjct 846   GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 905

Query 938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
          |||
Sbjct 906   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 965

Query 998   GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          |||
Sbjct 966   GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1025

Query 1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 1117
          |||
Sbjct 1026   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 1085

Query 1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||
Sbjct 1086   CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1145

Query 1178   GACGAGTTCTTCTGAG 1193
          |||
Sbjct 1146   GACGAGTTCTTCTGAG 1161
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>gb|AF416990.1| Synthetic construct plasmid pcDNA3-Rluc, complete sequence
Length=6394

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query   398      ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGCCGCTTGGGTGGAGAGGCTATTC 457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3099      ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGCCGCTTGGGTGGAGAGGCTATTC 3158

Query   458      GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3159      GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 3218

Query   518      GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAC TG 577
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3219      GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAC TG 3278

Query   578      CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG 637
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3279      CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG 3338

Query   638      CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3339      CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 3398

Query   698      GATCTCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3399      GATCTCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 3458

Query   758      CGGCGGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 817
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3459      CGGCGGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC 3518

Query   818      ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3519      ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 3578

Query   878      GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 937
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3579      GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 3638

Query   938      GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3639      GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 3698

Query   998      GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3699      GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 3758

Query   1058     ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 1117
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3759     ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 3818

Query   1118     CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3819     CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 3878

Query   1178     GACGAGTTCTTCTGAG 1193
          ||||||||||||||||
Sbjct   3879     GACGAGTTCTTCTGAG 3894

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>gb|AY181092.1| Synthetic construct S1 promoter-nptII gene-S3 terminator cassett
Length=1688

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query   398      ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGCCGCTTGGGTGGAGAGGCTATTC 457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   545      ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGCCGCTTGGGTGGAGAGGCTATTC 604

Query   458      GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   605      GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 664

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Query 518 GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577
          |||
Sbjct 665 GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 724

Query 578 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 637
          |||
Sbjct 725 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 784

Query 638 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
          |||
Sbjct 785 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 844

Query 698 GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          |||
Sbjct 845 GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 904

Query 758 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 817
          |||
Sbjct 905 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 964

Query 818 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
          |||
Sbjct 965 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 1024

Query 878 GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 937
          |||
Sbjct 1025 GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 1084


Query 938 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
          |||
Sbjct 1085 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 1144

Query 998 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          |||
Sbjct 1145 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1204

Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 1117
          |||
Sbjct 1205 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 1264

Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||
Sbjct 1265 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1324

Query 1178 GACGAGTTCTTCTGAG 1193
          |||
Sbjct 1325 GACGAGTTCTTCTGAG 1340
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>gb|AY159034.1|  Cloning vector pPLEX-4004, complete sequence
Length=12880

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query 398 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
          |||
Sbjct 11745 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 11804

Query 458 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          |||
Sbjct 11805 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 11864


Query 518 GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577
          |||
Sbjct 11865 GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 11924

Query 578 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 637
          |||
Sbjct 11925 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 11984

Query 638 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
          |||
Sbjct 11985 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 12044

Query 698 GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          |||
Sbjct 12045 GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 12104
```

Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCACCAAGCGAAACATCGC	817
Sbjct	12105	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCACCAAGCGAAACATCGC	12164
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	12165	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	12224
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC	937
Sbjct	12225	GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC	12284
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	997
Sbjct	12285	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	12344
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	12345	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	12404
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	1117
Sbjct	12405	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	12464
Query	1118	CTCGTGCTTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	12465	CTCGTGCTTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	12524
Query	1178	GACGAGTTCTTCTGAG	1193
Sbjct	12525	GACGAGTTCTTCTGAG	12540

>gb|AY159033.1|  Cloning vector pPLEX-4003, complete sequence
Length=12388

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTC	457
Sbjct	11253	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTC	11312
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	11313	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	11372
Query	518	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	11373	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	11432
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTG	637
Sbjct	11433	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTG	11492
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	11493	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	11552
Query	698	GATCTCCTGTCTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	11553	GATCTCCTGTCTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	11612
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCACCAAGCGAAACATCGC	817
Sbjct	11613	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCACCAAGCGAAACATCGC	11672
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	11673	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	11732
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC	937
Sbjct	11733	GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC	11792
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	997

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Sbjct  11793  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT 11852
Query   998      GGCCGCTTTTCTGGATTATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          |||
Sbjct  11853  GGCCGCTTTTCTGGATTATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 11912
Query  1058      ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 1117
          |||
Sbjct  11913  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 11972
Query  1118      CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||
Sbjct  11973  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 12032
Query  1178      GACGAGTTCTTCTGAG 1193
          |||
Sbjct  12033  GACGAGTTCTTCTGAG 12048

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>gb|AY159032.1|  Cloning vector pPLEX-4002, complete sequence
Length=12825


Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query   398      ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
          |||
Sbjct  11690  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 11749
Query   458      GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          |||
Sbjct  11750  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 11809
Query   518      GCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT 577
          |||
Sbjct  11810  GCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT 11869
Query   578      CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCTTGCGCAGCTGTG 637
          |||
Sbjct  11870  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCTTGCGCAGCTGTG 11929
Query   638      CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
          |||
Sbjct  11930  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 11989
Query   698      GATCTCCTGTTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          |||
Sbjct  11990  GATCTCCTGTTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 12049
Query   758      CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 817
          |||
Sbjct  12050  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 12109
Query   818      ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
          |||
Sbjct  12110  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 12169
Query   878      GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 937
          |||
Sbjct  12170  GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 12229
Query   938      GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT 997
          |||
Sbjct  12230  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT 12289
Query   998      GGCCGCTTTTCTGGATTATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          |||
Sbjct  12290  GGCCGCTTTTCTGGATTATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 12349
Query  1058      ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 1117
          |||
Sbjct  12350  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 12409
Query  1118      CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||
Sbjct  12410  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 12469
Query  1178      GACGAGTTCTTCTGAG 1193


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Sbjct 12470 |||||
GACGAGTTCTTCTGAG 12485

>gb|AY159031.1|  Cloning vector pPLEX-4001, complete sequence
Length=12377

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus


Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	11242	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	11301
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	11302	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	11361
Query	518	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	11362	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	11421
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTG	637
Sbjct	11422	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTG	11481
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	11482	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	11541
Query	698	GATCTCCTGTCTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	11542	GATCTCCTGTCTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	11601
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCAAGCGAAACATCGC	817
Sbjct	11602	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCAAGCGAAACATCGC	11661
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	11662	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	11721
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC	937
Sbjct	11722	GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC	11781
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	997
Sbjct	11782	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	11841
Query	998	GGCCGCTTTTCTGGATTATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	11842	GGCCGCTTTTCTGGATTATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	11901
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGGCTGACCGCTTC	1117
Sbjct	11902	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGGCTGACCGCTTC	11961
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	11962	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	12021
Query	1178	GACGAGTTCTTCTGAG 1193	
Sbjct	12022	GACGAGTTCTTCTGAG 12037	

>gb|AY159029.1|  Cloning vector pPLEX-501, complete sequence
Length=10858

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	9723	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	9782

Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	9783	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	9842
Query	518	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	9843	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	9902
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	637
Sbjct	9903	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	9962
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	9963	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	10022
Query	698	GATCTCCTGTCTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	10023	GATCTCCTGTCTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	10082
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCCACCAAGCGAAACATCGC	817
Sbjct	10083	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCCACCAAGCGAAACATCGC	10142
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	10143	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	10202
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC	937
Sbjct	10203	GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC	10262
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	997
Sbjct	10263	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	10322
Query	998	GGCCGCTTTTCTGGATTATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	10323	GGCCGCTTTTCTGGATTATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	10382
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGGCTGACCGCTTC	1117
Sbjct	10383	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGGCTGACCGCTTC	10442
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	10443	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	10502
Query	1178	GACGAGTTCTTCTGAG 1193	
Sbjct	10503	GACGAGTTCTTCTGAG 10518	

>gb|AY159020.1|  Cloning vector pPLEX-505, complete sequence
Length=10862

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	9727	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	9786
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	9787	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	9846
Query	518	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	9847	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	9906
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	637
Sbjct	9907	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	9966
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697

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Sbjct  9967   CTCGACGTTGTCACCTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  10026
Query  698     GATCTCCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
          |||
Sbjct  10027   GATCTCCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  10086
Query  758     CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
          |||
Sbjct  10087   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  10146
Query  818     ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
          |||
Sbjct  10147   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  10206
Query  878     GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  937
          |||
Sbjct  10207   GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  10266
Query  938     GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
          |||
Sbjct  10267   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  10326
Query  998     GGCCGCTTTTCTGGATTATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
          |||
Sbjct  10327   GGCCGCTTTTCTGGATTATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  10386
Query  1058    ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
          |||
Sbjct  10387    ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  10446
Query  1118    CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT  1177
          |||
Sbjct  10447    CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT  10506
Query  1178    GACGAGTTCTTCTGAG  1193
          |||
Sbjct  10507    GACGAGTTCTTCTGAG  10522
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>gb|AY048743.1| Template plasmid pKD4, complete sequence
Length=3267

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query  398     ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
          |||
Sbjct  459     ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  518
Query  458     GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
          |||
Sbjct  519     GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  578
Query  518     GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
          |||
Sbjct  579     GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  638
Query  578     CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
          |||
Sbjct  639     CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  698
Query  638     CTCGACGTTGTCACCTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
          |||
Sbjct  699     CTCGACGTTGTCACCTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  758
Query  698     GATCTCCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
          |||
Sbjct  759     GATCTCCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  818
Query  758     CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
          |||
Sbjct  819     CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  878
Query  818     ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
          |||
Sbjct  879     ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  938
Query  878     GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  937
          |||
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Sbjct  939  GAGCATCAGGGGCTCGCGCCAGCCGAAC TGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 998
Query  938  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
          |||
Sbjct  999  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 1058
Query  998  GGCCGCTTTTCTGGATTCAATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          |||
Sbjct  1059  GGCCGCTTTTCTGGATTCAATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1118
Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 1117
          |||
Sbjct  1119  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 1178
Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||
Sbjct  1179  CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT 1238
Query  1178  GACGAGTTCTTCTGAG 1193
          |||
Sbjct  1239  GACGAGTTCTTCTGAG 1254
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>gb|AY237648.1|  Cloning vector pHR50, complete sequence
Length=11973

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

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Query  398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
          |||
Sbjct  3776  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 3717
Query  458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          |||
Sbjct  3716  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 3657
Query  518  GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577
          |||
Sbjct  3656  GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 3597
Query  578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 637
          |||
Sbjct  3596  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 3537
Query  638  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
          |||
Sbjct  3536  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 3477
Query  698  GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          |||
Sbjct  3476  GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 3417
Query  758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 817
          |||
Sbjct  3416  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 3357
Query  818  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
          |||
Sbjct  3356  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 3297
Query  878  GAGCATCAGGGGCTCGCGCCAGCCGAAC TGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 937
          |||
Sbjct  3296  GAGCATCAGGGGCTCGCGCCAGCCGAAC TGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 3237
Query  938  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
          |||
Sbjct  3236  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 3177
Query  998  GGCCGCTTTTCTGGATTCAATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          |||
Sbjct  3176  GGCCGCTTTTCTGGATTCAATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 3117
Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 1117
          |||
Sbjct  3116  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 3057
Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
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Sbjct  3056  |||||
CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT  2997
Query  1178  GACGAGTTCTTCTGAG  1193
          |||||
Sbjct  2996  GACGAGTTCTTCTGAG  2981
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>gb|AY237649.1| Cloning vector pHR3-km, complete sequence
Length=6762

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

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Query  398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
          |||||
Sbjct  3776  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  3717
Query  458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
          |||||
Sbjct  3716  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  3657
Query  518  GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
          |||||
Sbjct  3656  GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  3597
Query  578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG  637
          |||||
Sbjct  3596  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG  3537
Query  638  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
          |||||
Sbjct  3536  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  3477
Query  698  GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
          |||||
Sbjct  3476  GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  3417
Query  758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC  817
          |||||
Sbjct  3416  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC  3357
Query  818  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
          |||||
Sbjct  3356  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  3297
Query  878  GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  937
          |||||
Sbjct  3296  GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  3237
Query  938  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT  997
          |||||
Sbjct  3236  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT  3177
Query  998  GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
          |||||
Sbjct  3176  GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  3117
Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC  1117
          |||||
Sbjct  3116  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC  3057
Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT  1177
          |||||
Sbjct  3056  CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT  2997
Query  1178  GACGAGTTCTTCTGAG  1193
          |||||
Sbjct  2996  GACGAGTTCTTCTGAG  2981
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>gb|AY265466.1| Shuttle vector pAM2770, complete sequence
Length=8384

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query  398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
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Sbjct	739	 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	798
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	799	 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	858
Query	518	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	859	 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	918
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	637
Sbjct	919	 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	978
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	979	 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	1038
Query	698	GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	1039	 GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	1098
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	817
Sbjct	1099	 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	1158
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	1159	 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	1218
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	937
Sbjct	1219	 GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	1278
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	997
Sbjct	1279	 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	1338
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	1339	 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1398
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	1117
Sbjct	1399	 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	1458
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	1459	 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1518
Query	1178	GACGAGTTCTTCTGAG 1193	
Sbjct	1519	 GACGAGTTCTTCTGAG 1534	

>gb|AF346624.1|AF346624 RAGE vector pRIG1, complete sequence
Length=6836

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	3847	 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	3906
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	3907	 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	3966
Query	518	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	3967	 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	4026
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	637
Sbjct	4027	 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTG	4086
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697

Sbjct	4087	 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	4146
Query	698	GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	4147	 GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	4206
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	817
Sbjct	4207	 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	4266
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	4267	 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	4326
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	937
Sbjct	4327	 GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	4386
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT	997
Sbjct	4387	 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT	4446
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	4447	 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	4506
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	1117
Sbjct	4507	 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	4566
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	4567	 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	4626
Query	1178	GACGAGTTCTTCTGAG 1193	
Sbjct	4627	 GACGAGTTCTTCTGAG 4642	

>emb|AL671256.1|TBN19B2  Trypanosoma brucei VO2 VSG expression site BAC
Length=137759

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	117684	 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	1177
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	117744	 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	1178
Query	518	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	117804	 GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	1178
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTTCGCGAGCTGTG	637
Sbjct	117864	 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTTCGCGAGCTGTG	1179
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	117924	 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	1179
Query	698	GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	117984	 GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	1180
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	817
Sbjct	118044	 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	1181
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	118104	 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	1181

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Query 878      GAGCATCAGGGGCTCGCGCCAGCCGAAC TGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 937
Sbjct 118164   GAGCATCAGGGGCTCGCGCCAGCCGAAC TGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 1182

Query 938      GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
Sbjct 118224   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 1182

Query 998      GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
Sbjct 118284   GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1183

Query 1058     ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 1117
Sbjct 118344   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 1184

Query 1118     CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
Sbjct 118404   CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1184

Query 1178     GACGAGTTCTTCTGAG 1193
Sbjct 118464   GACGAGTTCTTCTGAG 118479
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>gb|AF286462.1|AF286462 Promoter probe vector pPROBE'-gfp[LVA], complete sequenc
Length=7385

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

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Query 398      ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
Sbjct 6928     ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 6869

Query 458      GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
Sbjct 6868     GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 6809

Query 518      GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAC TG 577
Sbjct 6808     GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAC TG 6749

Query 578      CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 637
Sbjct 6748     CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 6689

Query 638      CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
Sbjct 6688     CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 6629

Query 698      GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
Sbjct 6628     GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 6569

Query 758      CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 817
Sbjct 6568     CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 6509

Query 818      ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
Sbjct 6508     ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 6449

Query 878      GAGCATCAGGGGCTCGCGCCAGCCGAAC TGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 937
Sbjct 6448     GAGCATCAGGGGCTCGCGCCAGCCGAAC TGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 6389

Query 938      GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
Sbjct 6388     GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 6329

Query 998      GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
Sbjct 6328     GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 6269

Query 1058     ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 1117
Sbjct 6268     ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 6209
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Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||
Sbjct 6208 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 6149

Query 1178 GACGAGTTCTTCTGAG 1193
          |||
Sbjct 6148 GACGAGTTCTTCTGAG 6133
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>gb|AF286461.1|AF286461 Promoter probe vector pPROBE-gfp[LVA], complete sequence
Length=7382

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

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Query 398 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
          |||
Sbjct 6925 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 6866

Query 458 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          |||
Sbjct 6865 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 6806

Query 518 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACCTG 577
          |||
Sbjct 6805 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACCTG 6746

Query 578 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 637
          |||
Sbjct 6745 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 6686

Query 638 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
          |||
Sbjct 6685 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 6626

Query 698 GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          |||
Sbjct 6625 GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 6566

Query 758 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 817
          |||
Sbjct 6565 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 6506

Query 818 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
          |||
Sbjct 6505 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 6446

Query 878 GAGCATCAGGGGCTCGCGCCAGCCGAACCTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC 937
          |||
Sbjct 6445 GAGCATCAGGGGCTCGCGCCAGCCGAACCTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC 6386

Query 938 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
          |||
Sbjct 6385 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 6326

Query 998 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          |||
Sbjct 6325 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 6266

Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGGCTGACCGCTTC 1117
          |||
Sbjct 6265 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGGCTGACCGCTTC 6206

Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||
Sbjct 6205 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 6146

Query 1178 GACGAGTTCTTCTGAG 1193
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>gb|AF286460.1|AF286460 Promoter probe vector pPROBE'-gfp[ASV], complete sequence
Length=7385

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

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Query 398 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 6928 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 6869

Query 458 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 6868 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 6809

Query 518 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 6808 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 6749

Query 578 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCAGCTGTG 637
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 6748 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCAGCTGTG 6689

Query 638 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 6688 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 6629

Query 698 GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 6628 GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 6569

Query 758 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 817
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 6568 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 6509

Query 818 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 6508 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 6449

Query 878 GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC 937
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Sbjct 6448 GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC 6389

Query 938 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 6388 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 6329

Query 998 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 6328 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 6269

Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 1117
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 6268 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 6209

Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 6208 CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT 6149

Query 1178 GACGAGTTCTTCTGAG 1193
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Sbjct 6148 GACGAGTTCTTCTGAG 6133
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>gb|AF286459.1|AF286459 Promoter probe vector pPROBE-gfp[ASV], complete sequence
Length=7382

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

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Query 398 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 6925 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 6866

Query 458 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 6865 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 6806

Query 518 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 6805 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 6746

Query 578 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCAGCTGTG 637
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 6745 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCAGCTGTG 6686
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Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	6685	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	6626
Query	698	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	6625	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	6566
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCACCAAGCGAAACATCGC	817
Sbjct	6565	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCACCAAGCGAAACATCGC	6506
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	6505	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	6446
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	937
Sbjct	6445	GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	6386
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	997
Sbjct	6385	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	6326
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	6325	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	6266
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	1117
Sbjct	6265	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	6206
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	6205	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	6146
Query	1178	GACGAGTTCTTCTGAG	1193
Sbjct	6145	GACGAGTTCTTCTGAG	6130

>gb|AF286458.1|AF286458 Promoter probe vector pPROBE'-gfp[AAV], complete sequenc
Length=7385

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTC	457
Sbjct	6928	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTC	6869
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	6868	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	6809
Query	518	GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	6808	GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	6749
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	637
Sbjct	6748	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	6689
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	6688	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	6629
Query	698	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	6628	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	6569
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCACCAAGCGAAACATCGC	817
Sbjct	6568	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCACCAAGCGAAACATCGC	6509
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	6508	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	6449

Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAAC	937
Sbjct	6448	GAGCATCAGGGGCTCGCGCCAGCCGAAC	6389
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCTTGCCGAATATCATGGTGGAAAAAT	997
Sbjct	6388	GGCGAGGATCTCGTCGTGACCCATGGCGATGCTTGCCGAATATCATGGTGGAAAAAT	6329
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	6328	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	6269
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	1117
Sbjct	6268	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	6209
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	6208	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	6149
Query	1178	GACGAGTTCTTCTGAG	1193
Sbjct	6148	GACGAGTTCTTCTGAG	6133

>gb|AF286457.1|AF286457 Promoter probe vector pPROBE-gfp[AAV], complete sequence
Length=7382

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	6925	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	6866
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	6865	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	6806
Query	518	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	6805	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	6746
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	637
Sbjct	6745	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	6686
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	6685	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	6626
Query	698	GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	6625	GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	6566
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	817
Sbjct	6565	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	6506
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	6505	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	6446
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAAC	937
Sbjct	6445	GAGCATCAGGGGCTCGCGCCAGCCGAAC	6386
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCTTGCCGAATATCATGGTGGAAAAAT	997
Sbjct	6385	GGCGAGGATCTCGTCGTGACCCATGGCGATGCTTGCCGAATATCATGGTGGAAAAAT	6326
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	6325	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	6266
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	1117
Sbjct	6265	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	6206

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Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||
Sbjct 6205 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 6146

Query 1178 GACGAGTTCTTCTGAG 1193
          |||
Sbjct 6145 GACGAGTTCTTCTGAG 6130
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>gb|AF286456.1|AF286456 Promoter probe vector pPROBE'-gfp[tagless], complete seq
Length=7343

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

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Query 398 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGCCGCTTGGGTGGAGAGGCTATTC 457
          |||
Sbjct 6886 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGCCGCTTGGGTGGAGAGGCTATTC 6827

Query 458 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          |||
Sbjct 6826 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 6767

Query 518 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACCTG 577
          |||
Sbjct 6766 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACCTG 6707

Query 578 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 637
          |||
Sbjct 6706 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 6647

Query 638 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
          |||
Sbjct 6646 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 6587

Query 698 GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          |||
Sbjct 6586 GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 6527

Query 758 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 817
          |||
Sbjct 6526 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 6467

Query 818 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
          |||
Sbjct 6466 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 6407

Query 878 GAGCATCAGGGGCTCGCGCCAGCCGAACCTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC 937
          |||
Sbjct 6406 GAGCATCAGGGGCTCGCGCCAGCCGAACCTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC 6347

Query 938 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
          |||
Sbjct 6346 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 6287

Query 998 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          |||
Sbjct 6286 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 6227

Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGGCTGACCGCTTC 1117
          |||
Sbjct 6226 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGGCTGACCGCTTC 6167

Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||
Sbjct 6166 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 6107

Query 1178 GACGAGTTCTTCTGAG 1193
          |||
Sbjct 6106 GACGAGTTCTTCTGAG 6091
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>gb|AF286455.1|AF286455 Promoter probe vector pPROBE-gfp[tagless], complete sequ
Length=7340

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	6883	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	6824
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	6823	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	6764
Query	518	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	6763	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	6704
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG	637
Sbjct	6703	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG	6644
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	6643	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	6584
Query	698	GATCTCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	6583	GATCTCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	6524
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	817
Sbjct	6523	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC	6464
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	6463	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	6404
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC	937
Sbjct	6403	GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC	6344
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	997
Sbjct	6343	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	6284
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	6283	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	6224
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	1117
Sbjct	6223	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC	6164
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	6163	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	6104
Query	1178	GACGAGTTCTTCTGAG	1193
Sbjct	6103	GACGAGTTCTTCTGAG	6088

>gb|AF286454.1|AF286454 Promoter probe vector pPROBE-NT', complete sequence
Length=6810

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	457
Sbjct	6353	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC	6294
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	6293	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	6234
Query	518	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	6233	GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	6174
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG	637
Sbjct	6173	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG	6114

Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	6113	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	6054
Query	698	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	6053	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	5994
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCACCAAGCGAAACATCGC	817
Sbjct	5993	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCACCAAGCGAAACATCGC	5934
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	5933	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	5874
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	937
Sbjct	5873	GAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTGCCAGGCTCAAGGCGCGCATGCCCGAC	5814
Query	938	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	997
Sbjct	5813	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGAAAAAT	5754
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	5753	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	5694
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	1117
Sbjct	5693	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	5634
Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
Sbjct	5633	CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT	5574
Query	1178	GACGAGTTCTTCTGAG	1193
Sbjct	5573	GACGAGTTCTTCTGAG	5558

>gb|AF286453.1|AF286453 Promoter probe vector pPROBE-NT, complete sequence
Length=6807

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTC	457
Sbjct	6350	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTC	6291
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	6290	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	6231
Query	518	GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	6230	GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	6171
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	637
Sbjct	6170	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG	6111
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	6110	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	6051
Query	698	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	6050	GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	5991
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCACCAAGCGAAACATCGC	817
Sbjct	5990	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGACCACCAAGCGAAACATCGC	5931
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	5930	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	5871

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Query 878 GAGCATCAGGGGCTCGCGCCAGCCGAAC TGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 937
      |||
Sbjct 5870 GAGCATCAGGGGCTCGCGCCAGCCGAAC TGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 5811

Query 938 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
      |||
Sbjct 5810 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 5751

Query 998 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
      |||
Sbjct 5750 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 5691

Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 1117
      |||
Sbjct 5690 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 5631

Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
      |||
Sbjct 5630 CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT 5571

Query 1178 GACGAGTTCTTCTGAG 1193
      |||
Sbjct 5570 GACGAGTTCTTCTGAG 5555
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>gb|AY962288.1| Low threshold vector pLTSUB-302, complete sequence
Length=4719

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query 398 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
      |||
Sbjct 3103 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 3162

Query 458 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
      |||
Sbjct 3163 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 3222

Query 518 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577
      |||
Sbjct 3223 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 3282

Query 578 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 637
      |||
Sbjct 3283 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 3342

Query 638 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
      |||
Sbjct 3343 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 3402

Query 698 GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
      |||
Sbjct 3403 GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 3462

Query 758 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 817
      |||
Sbjct 3463 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 3522

Query 818 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
      |||
Sbjct 3523 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 3582

Query 878 GAGCATCAGGGGCTCGCGCCAGCCGAAC TGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 937
      |||
Sbjct 3583 GAGCATCAGGGGCTCGCGCCAGCCGAAC TGTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC 3642

Query 938 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
      |||
Sbjct 3643 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 3702

Query 998 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
      |||
Sbjct 3703 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 3762

Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 1117
      |||
Sbjct 3763 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 3822
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Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||
Sbjct 3823 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 3882

Query 1178 GACGAGTTCTTCTGAG 1193
          |||
Sbjct 3883 GACGAGTTCTTCTGAG 3898
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>gb|AY952935.1| Expression vector pFNK-101, complete sequence
Length=4099

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

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Query 398 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
          |||
Sbjct 4020 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 3961

Query 458 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
          |||
Sbjct 3960 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 3901

Query 518 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT 577
          |||
Sbjct 3900 GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT 3841

Query 578 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 637
          |||
Sbjct 3840 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 3781

Query 638 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
          |||
Sbjct 3780 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 3721

Query 698 GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
          |||
Sbjct 3720 GATCTCCTGTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 3661

Query 758 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 817
          |||
Sbjct 3660 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 3601

Query 818 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
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Sbjct 3600 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 3541

Query 878 GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 937
          |||
Sbjct 3540 GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 3481

Query 938 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 997
          |||
Sbjct 3480 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT 3421

Query 998 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
          |||
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Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 1117
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Sbjct 3360 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 3301

Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 1177
          |||
Sbjct 3300 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT 3241

Query 1178 GACGAGTTCTTCTGAG 1193
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Sbjct 3240 GACGAGTTCTTCTGAG 3225
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>gb|AY952936.1| Expression vector pINV-110, complete sequence
Length=4887

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
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Sbjct   4751   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   4692

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
          |||
Sbjct   4691   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   4632

Query   518   GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT   577
          |||
Sbjct   4631   GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT   4572

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG   637
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Sbjct   4571   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG   4512

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
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Sbjct   4511   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   4452

Query   698   GATCTCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
          |||
Sbjct   4451   GATCTCTGTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   4392

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
          |||
Sbjct   4391   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   4332

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
          |||
Sbjct   4331   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   4272

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
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Sbjct   4271   GAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   4212

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT   997
          |||
Sbjct   4211   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT   4152


Query   998   GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
          |||
Sbjct   4151   GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   4092

Query   1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
          |||
Sbjct   4091   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   4032

Query   1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT   1177
          |||
Sbjct   4031   CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT   3972

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>gb|DQ225747.1|  Gene trapping Ds/T-DNA vector pUR224NB, complete sequence
Length=22828

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
          |||
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Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
          |||
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Query   518   GCGCAGGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT   577
          |||
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Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTG   637
          |||
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Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	4899	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	4958
Query	698	GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	4959	GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	5018
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	817
Sbjct	5019	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	5078
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877
Sbjct	5079	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	5138
Query	878	GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC	937
Sbjct	5139	GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTTCGCCAGGCTCAAGGCGCGCATGCCCCGAC	5198
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Sbjct	5199	GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT	5258
Query	998	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	1057
Sbjct	5259	GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC	5318
Query	1058	ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC	1117
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Query	1118	CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTT	1177
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>gb|DQ225746.1|  Gene trapping Ds/T-DNA vector pUR224NA, complete sequence
Length=22828

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

Query	398	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTC	457
Sbjct	8509	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTC	8450
Query	458	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	517
Sbjct	8449	GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA	8390
Query	518	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	577
Sbjct	8389	GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG	8330
Query	578	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTG	637
Sbjct	8329	CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTG	8270
Query	638	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	697
Sbjct	8269	CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG	8210
Query	698	GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	757
Sbjct	8209	GATCTCCTGTCACTCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG	8150
Query	758	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	817
Sbjct	8149	CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCACCAAGCGAAACATCGC	8090
Query	818	ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA	877


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Sbjct  8089  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  8030
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Query  938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
          |||
Sbjct  7969  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  7910
Query  998   GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
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Sbjct  7909  GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  7850
Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
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Sbjct  7849  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  7790
Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT  1177
          |||
Sbjct  7789  CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTT  7730
Query  1178  GACGAGTTCTTCTGAG  1193
          |||
Sbjct  7729  GACGAGTTCTTCTGAG  7714
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